

141606

STIC-Biotech/ChemLib

From: Bunner, Bridget  
Sent: Monday, January 03, 2005 12:49 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search

Hi! I'd like a sequence search performed for case 10/086,177:

1. the amino acid sequence of SEQ ID NO: 12
2. the amino acid sequence of SEQ ID NO: 13

CRAFE

Thanks!

Bridget Bunner

Art Unit 1647  
Rem 4C65  
(571) 272-0881  
mailbox 4C70

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: 1/5/05  
Date Completed: 1/5/05  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence : # 2  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: QAP  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

*This Page Blank (uspro)*

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 15:43:59 ; Search time 27.3508 Seconds  
(without alignments)  
73.553 Million cell updates/sec

Title: US-10-086-177A-13

Perfect score: 175

Sequence: 1 KPVSLSYRCPCRFPGGGLKWIQIYLEKALN 31

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*

2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*

3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*

4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*

5: /cgn2\_6/ptodata/1/1aa/PTCUS.COMB.pep:\*

6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	167	95.4	31	4	US-09-543-940-5
2	155	88.6	27	4	US-09-543-940-4
3	132	75.4	25	4	US-09-543-940-6
4	123	70.3	27	4	US-09-543-940-7
5	117	66.9	89	1	US-08-181-556-2
6	117	66.9	89	1	US-08-323-084A-1
7	117	66.9	89	1	US-08-674-008-1
8	117	66.9	89	4	US-09-461-912A-46
9	117	66.9	93	1	US-08-323-084A-5
10	117	66.9	93	1	US-08-674-008-5
11	117	66.9	93	4	US-09-312-283C-421
12	117	66.9	93	4	US-09-919-497-95
13	117	66.9	166	4	US-09-646-028-5
14	117	66.9	177	4	US-09-646-028-54
15	117	66.9	326	3	US-08-808-720-3
16	117	66.9	326	4	US-09-467-638-3
17	117	66.9	328	3	US-08-808-720-1
18	117	66.9	328	4	US-09-467-638-1
19	117	66.9	339	4	US-09-646-028-55
20	82	46.9	14	4	US-09-543-940-10
21	69	39.4	13	4	US-09-543-940-9
22	62	35.4	10	4	US-09-543-940-8
23	61	34.9	1084	4	US-09-221-013A-8
24	60.5	34.6	974	3	US-08-960-048-6
25	60.5	34.6	974	4	US-08-938-586-6
26	58	33.1	535	4	US-09-252-991A-25662
27	57	32.6	97	4	US-09-270-767-39706

28	57	32.6	97	4	US-09-270-767-54923	Sequence 54923, A
29	57	32.6	122	4	US-09-270-767-32013	Sequence 32013, A
30	57	32.6	132	4	US-09-270-767-47230	Sequence 47230, A
31	56	32.0	701	4	US-09-248-796A-15250	Sequence 15250, A
32	55	31.4	10	4	US-09-543-940-12	Sequence 12, Appl
33	53	30.3	484	4	US-09-489-039A-9532	Sequence 9532, Ap
34	50	28.6	588	3	US-08-481-190-16	Sequence 16, Appl
35	50	28.6	588	5	PCT-US93-00869-16	Sequence 16, Appl
36	50	28.6	685	3	US-08-960-048-7	Sequence 7, Appl
37	50	28.6	685	4	US-09-838-586-7	Sequence 7, Appl
38	49.5	28.3	504	4	US-09-252-991A-32272	Sequence 32272, A
39	49	28.0	416	1	US-08-117-083-61	Sequence 61, Appl
40	49	28.0	488	4	US-08-311-731A-29	Sequence 29, Appl
41	48	27.4	78	3	US-09-188-930-158	Sequence 158, App
42	48	27.4	78	3	US-09-188-930-285	Sequence 285, App
43	48	27.4	78	4	US-09-312-283C-158	Sequence 158, App
44	48	27.4	78	4	US-09-312-283C-285	Sequence 285, App
45	48	27.4	125	3	US-08-722-126A-7	Sequence 7, Appl

## ALIGNMENTS

```
RESULT 1
US-09-543-940-5
Sequence 5, Application US/09543940
Patent No. 6613742
GENERAL INFORMATION:
APPLICANT: Huang, Ziwei
APPLICANT: Luo, Zhaoen
APPLICANT: Zhou, Naiping
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
FILE REFERENCE: 8321-40
CURRENT APPLICATION NUMBER: US/09/543,940
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,106
PRIOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide containing segments from N- and C-terminal
US-09-543-940-5

Query Match 95.4%; Score 167, DB 4, Length 31;
Best Local Similarity 96.8%; Pred. No. 5, 2e-16;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGLKWIQIYLEKALN 31
DB 1 KPVSLSYRCPCRFPGGGLKWIQIYLEKALN 31

RESULT 2
US-09-543-940-4
Sequence 4, Application US/09543940
Patent No. 6613742
GENERAL INFORMATION:
APPLICANT: Huang, Ziwei
APPLICANT: Luo, Zhaoen
APPLICANT: Zhou, Naiping
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
FILE REFERENCE: 8321-40
CURRENT APPLICATION NUMBER: US/09/543,940
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,106
```

PRIOR FILING DATE: 1999-04-07  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 27  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide containing segments from N- and C-terminal  
OTHER INFORMATION: regions of human SDF-1 protein  
US-09-543-940-4

Query Match 88.6%; Score 155; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.9e-14;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LSTRCPFRFGGGLKWIQIYLEKALN 31  
DB 1 LSTRCPFRFGGGLKWIQIYLEKALN 27

RESULT 3  
US-09-543-940-6  
Sequence 6, Application US/09543940  
Patent No. 6613742  
GENERAL INFORMATION:  
APPLICANT: Huang, Ziwel  
APPLICANT: Luo, Zhaowen  
APPLICANT: Zhou, Naiping  
APPLICANT: Luo, Jiansong  
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides  
FILE REFERENCE: 8321-40  
CURRENT APPLICATION NUMBER: US/09/543,940  
CURRENT FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: 60/128,106  
PRIOR FILING DATE: 1999-04-07  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide containing segments from N- and C-terminal  
OTHER INFORMATION: regions of human SDF-1 protein  
US-09-543-940-6

Query Match 75.4%; Score 132; DB 4; Length 25;  
Best Local Similarity 92.6%; Pred. No. 2.5e-11;  
Matches 25; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 5 LSTRCPFRFGGGLKWIQIYLEKALN 31  
DB 1 LSTRCPFRFGGGLKWIQIYLEKALN 25

RESULT 4  
US-09-543-940-7  
Sequence 7, Application US/09543940  
Patent No. 6613742  
GENERAL INFORMATION:  
APPLICANT: Huang, Ziwel  
APPLICANT: Luo, Zhaowen  
APPLICANT: Zhou, Naiping  
APPLICANT: Luo, Jiansong  
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides  
FILE REFERENCE: 8321-40  
CURRENT APPLICATION NUMBER: US/09/543,940  
CURRENT FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: 60/128,106  
PRIOR FILING DATE: 1999-04-07

NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 27  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide containing segments from N- and C-terminal  
OTHER INFORMATION: regions of human SDF-1 protein  
US-09-543-940-7

Query Match 70.3%; Score 123; DB 4; Length 27;  
Best Local Similarity 85.2%; Pred. No. 4.5e-10;  
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 LSTRCPFRFGGGLKWIQIYLEKALN 31  
DB 1 LSTRCPFRFGGGLKWIQIYLEKALN 27

RESULT 5  
US-08-181-556-2  
Sequence 2, Application US/08181556  
Patent No. 5525486  
GENERAL INFORMATION:  
APPLICANT: HONTO, Tsauku  
APPLICANT: TASHIRO, Kei  
APPLICANT: TADA, Hideaki  
TITLE OF INVENTION: PROCESS FOR CONSTRUCTING cDNA LIBRARY,  
TITLE OF INVENTION: AND NOVEL POLYPEPTIDE AND DNA CODING FOR THE SAME  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STEVENS, DAVIS, MILLER & MOSHER  
STREET: 515 No. 5525486th Washington Street (P.O. Box 1427)  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22313  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/181,556  
FILING DATE: 14-JAN-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-22098  
FILING DATE: 14-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: POULOS III, James A.  
REGISTRATION NUMBER: 31714  
REFERENCE/DOCKET NUMBER: TTP/29088  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 549-7200  
TELEFAX: (703) 528-5313  
TELEX: 88-2746  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 89 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-181-556-2

Query Match 66.9%; Score 117; DB 1; Length 89;  
Best Local Similarity 40.3%; Pred. No. 1e-08;  
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;  
QY 1 KPVSLSTRCPFRFGG-----GGLKWIQI 24  
|||||

Db 22 KPVSLSTRCPREFSHIARANYHKLINTPNCALQIVARLKNNNQVCIDPRLKXIOE 81  
QY 25 YLEKALN 31  
82 YLEKALN 88

## RESULT 6

US-08-323-084A-1  
Sequence 1, Application US/08323084A  
Patent No. 5563048  
GENERAL INFORMATION:  
APPLICANT: HONJO, TASHIKU  
APPLICANT: SHIROZU, MICHIO  
APPLICANT: TADA, HIDEAKI  
TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/323,084A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 280505/1993  
FILING DATE: 14-OCT-1993  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 89 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-323-084A-1

Query Match 66.9%; Score 117; DB 1; Length 89;  
Best Local Similarity 40.3%; Pred. No. 1e-08;  
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSTRCPREFSG-----GGKXIOE 24  
Db 22 KPVSLSTRCPREFSHIARANYHKLINTPNCALQIVARLKNNNQVCIDPRLKXIOE 81  
QY 25 YLEKALN 31  
82 YLEKALN 88

## RESULT 7

US-08-674-008-1  
Sequence 1, Application US/08674008  
Patent No. 5756084  
GENERAL INFORMATION:  
APPLICANT: HONJO, Tashiku  
APPLICANT: SHIROZU, Michio  
APPLICANT: TADA, Hideaki  
TITLE OF INVENTION: HUMAN STROMAL DERIVED  
FACTOR 1 AND 1 (As Amended)  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/674,008  
FILING DATE: 1-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/323,084  
FILING DATE: 14-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 280505/1993  
FILING DATE: 14-OCT-1993  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 89 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-674-008-1

Query Match 66.9%; Score 117; DB 1; Length 89;  
Best Local Similarity 40.3%; Pred. No. 1e-08;  
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSTRCPREFSG-----GGKXIOE 24  
Db 22 KPVSLSTRCPREFSHIARANYHKLINTPNCALQIVARLKNNNQVCIDPRLKXIOE 81  
QY 25 YLEKALN 31  
82 YLEKALN 88

## RESULT 8

US-09-461-912A-46  
Sequence 46, Application US/09461912A  
Patent No. 6709855  
GENERAL INFORMATION:  
APPLICANT: Stanton, Lawrence A.  
APPLICANT: White, R. Tyler  
APPLICANT: Damm, Deborah L.  
APPLICANT: Lewicki, John A.  
TITLE OF INVENTION: Methods for detection and use of  
FILE REFERENCE: SCIOS.011A  
CURRENT APPLICATION NUMBER: US/09/461,912A  
PRIOR FILING DATE: 1999-12-15  
PRIOR APPLICATION NUMBER: US 60/113,008  
PRIOR FILING DATE: 1998-12-18  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 46  
LENGTH: 89  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-461-912A-46

Query Match 66.9%; Score 117; DB 4; Length 89;  
Best Local Similarity 40.3%; Pred. No. 1e-08;  
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

US-09-312-283C-421

Query March	66.9%;	Score 117;	DB 4;	Length 93;
Best Local Similarity	40.3%;	Pred. No. 1e-08;		
Matches 27;	Conservative 0;	Mismatches 4;	Indels 36;	Gaps 1;

**DQ** 1 KPVSLSYRCRCRFFGG-----GGLKWIQE 24  
**DQ** 22 KPVLSYRCRCRPFESHIAKAVNKHKLINTPNCALQIVARLKNRRQCVIDPKLKWIOE 81

Qy	25	YLEKALN	31
Db	82	YLEKALN	88

RESULT 12  
US-09-919

```

US-09-919-497-95
/ Sequence 95, Application US/09919497
/ Patent No. 6773883
/ GENERAL INFORMATION:
/ APPLICANT: Muller, George L.
/ TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
/ FILE REFERENCE: B0901/7225
/ CURRENT APPLICATION NUMBER: US/09/919,497
/ CURRENT FILING DATE: 2001-07-31
/ PRIOR APPLICATION NUMBER: US 60/221,735
/ PRIOR FILING DATE: 2000-07-31
/ NUMBER OF SEQ ID NOS: 100
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 95
/ LENGTH: 93
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-09-919-497-95

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Query Match	66.9%;	Score 117;	DB 4;	Length 93;
Best Local Similarity	40.3%;	Pred. No. 1e-08;		
Matches 27;	Conservative	0;	Mismatches 4;	Indels 36;
				Gaps 1;

**Qy** 1 KPVSLSYRCPCRPFGG-----GGLKVIQE 24  
**Dd** 22 KPVSLSYRCPCRFESHVARAVNKLKILNTPNCALQI VARLKNNNRQVCIDPKLVIOE 81	

QY	25	YLEKALN	31
Db	82	YLEKALN	88

RESULT 13  
US-09-646

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? Sequence 5, Application US/09646028
? Patent No. 6563347
?
? GENERAL INFORMATION:
?
? APPLICANT: Kwak, Larry
? APPLICANT: Birsagyt, Arya
? TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
? TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
? FILE REFERENCE: 14014.0316/P
? CURRENT APPLICATION NUMBER: US/09/646,028
? CURRENT FILING DATE: 2000-09-12
? PRIOR APPLICATION NUMBER: 60/077,745
? PRIOR FILING DATE: 1998-03-12
?
? NUMBER OF SEQ ID NOS: 57
?
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 5
? LENGTH: 166
?
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of artificial sequence: /note=synthetic construct
?
? US-09-646-028-5

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Query Match	66.9%	Score 117;	DB 4;	Length 166;
Best Local Similarity	40.3%	Pred. No. 1.9e-08;		
Matches	27;	Conservative	0;	Mismatches 4;
				Indels 36;
				Gaps 1

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QY      1 KPVSLSYRCPCRFEGS-----GGLKWIQE 24
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        |||||
DB     22 KPVLSYRCPCRFFESHVARPNVKHLKLINTPNCALQIVARLKNNNRQVCIDPKLKIQE 81
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QY	25	YLEKALN	31
Db	82	YLEKALN	88

RESULT 14  
US-09-646

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Sequence 54, Application us/09646028
Patent No. 6562347
GENERAL INFORMATION:
APPLICANT: Kwak, Larry
APPLICANT: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
FILE REFERENCE: 14014.0316/P
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: us/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIORITY FILING DATE: 1998-03-12
PRIORITY FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 54
LENGTH: 177
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-54

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Query Match	66.9%	Score 117;	DB 4;	Length 177;
Best Local Similarity	40.3%	Pred. No. 2e-08;		
Matches 27; Conservative	0;	Mismatches 4;	Indels 36;	Gaps 1;

Oy I KPVSLSYRCPGRFFGG-----GGLKWIQE 24  
Db 4 KPVSLSYRCGRFFESHVARANVKHLKLINTPCALQIVARLKNNNRQVCIDPKLKIQE 63

QY	25	YLEKALN	31
Db	64	YLEKALN	70

RESULT 15  
US-08-808

Sequence 3, Application US/08808720  
Patent No. 6100387  
GENERAL INFORMATION:  
APPLICANT: Herrmann, Steve  
APPLICANT: Swabberg, Stephen  
TITLE OF INVENTION: CHEMERIC POLYPEPTIDES CONTAINING  
TITLE OF INVENTION: CHEMOKINE DOMAINS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark  
CITY: Cambridge  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/808,720  
FILING DATE:  
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: Sprunger, Suzanne  
REGISTRATION NUMBER: P-41,323  
REFERENCE/DOCKET NUMBER: G15291  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8284  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 326 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-808-720-3

Query Match 66.9%; Score 117; DB 3; Length 326;  
Best Local Similarity 40.3%; Pred. No. 3.7e-08;  
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY	1	KPVSLSYRCPCRFPGG-----GGLKWTIOE	24
DB	20	KPVSLSYRCPCRFESHVAPANVGHKLINTPNCALQIVARLKNNNRQVCIDPRLKWTIOE	79
QY	25	YLEKALN	31
DB	80	YLEKALN	86

Search completed: January 4, 2005, 15:47:50  
Job time: 28.9508 secs



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## OM protein - protein search, using sw model

Run on: January 4, 2005, 15:46:58 ; Search time 101.131 Seconds

(without alignments)  
110.268 Million cell updates/sec

Title: US-10-086-177A-13

Perfect score: 175  
Sequence: 1 KPVSLSYRCPFRFGGGLKMTQIEYLKALN 31Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*

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11: /cgn2\_6/ptodata/1/pubppaa/US09C\_NEW\_PUB.pep:\*

12: /cgn2\_6/ptodata/1/pubppaa/US09C\_PUBCOMB.pep:\*

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17: /cgn2\_6/ptodata/1/pubppaa/US10C\_PUBCOMB.pep:\*

18: /cgn2\_6/ptodata/1/pubppaa/US11\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/1/pubppaa/US11\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	175	100.0	31 9 US-09-835-107-13	Sequence 13, App1
2	175	100.0	31 9 US-09-835-107-15	Sequence 15, App1
3	175	100.0	31 9 US-09-835-107-20	Sequence 20, App1
4	175	100.0	31 9 US-09-835-107-21	Sequence 21, App1
5	175	100.0	31 9 US-09-835-107-22	Sequence 22, App1
6	175	100.0	31 9 US-09-835-107-23	Sequence 23, App1
7	175	100.0	31 9 US-09-835-107-26	Sequence 26, App1
8	175	100.0	31 9 US-09-835-107-27	Sequence 27, App1
9	175	100.0	31 14 US-10-086-177A-13	Sequence 13, App1
10	175	100.0	31 14 US-10-086-177A-15	Sequence 15, App1
11	175	100.0	31 14 US-10-086-177A-20	Sequence 20, App1
12	175	100.0	31 14 US-10-086-177A-21	Sequence 21, App1
13	175	100.0	31 14 US-10-086-177A-22	Sequence 22, App1

14	175	100.0	31 14 US-10-086-177A-23	Sequence 23, App1
15	175	100.0	31 14 US-10-086-177A-26	Sequence 26, App1
16	175	100.0	31 14 US-10-086-177A-27	Sequence 27, App1
17	175	98.3	31 9 US-09-835-107-24	Sequence 24, App1
18	172	98.3	31 9 US-09-835-107-25	Sequence 25, App1
19	172	98.3	31 14 US-10-086-177A-24	Sequence 24, App1
20	172	98.3	31 14 US-10-086-177A-25	Sequence 25, App1
21	166	94.9	31 9 US-09-852-424-74	Sequence 74, App1
22	166	94.9	31 9 US-09-852-424-122	Sequence 122, App1
23	166	94.9	31 9 US-09-852-424-124	Sequence 124, App1
24	166	94.9	31 9 US-09-852-424-133	Sequence 133, App1
25	166	94.9	31 9 US-09-852-424-134	Sequence 134, App1
26	166	94.9	31 9 US-09-852-424-135	Sequence 135, App1
27	163.5	93.4	34 9 US-09-835-107-17	Sequence 17, App1
28	163.5	93.4	34 9 US-09-835-107-19	Sequence 19, App1
29	163.5	93.4	34 14 US-10-086-177A-17	Sequence 17, App1
30	163.5	93.4	34 14 US-10-086-177A-19	Sequence 19, App1
31	162	92.6	31 9 US-09-852-424-95	Sequence 95, App1
32	161	92.0	31 9 US-09-852-424-79	Sequence 79, App1
33	161	92.0	31 9 US-09-852-424-94	Sequence 94, App1
34	160	91.4	31 9 US-09-852-424-97	Sequence 97, App1
35	159	90.9	31 9 US-09-852-424-78	Sequence 78, App1
36	159	90.9	31 9 US-09-852-424-81	Sequence 81, App1
37	158.5	90.6	30 9 US-09-835-107-12	Sequence 12, App1
38	158.5	90.6	30 9 US-09-835-107-14	Sequence 14, App1
39	158.5	90.6	30 14 US-10-086-177A-12	Sequence 12, App1
40	158.5	90.6	30 14 US-10-086-177A-14	Sequence 14, App1
41	158	90.3	31 9 US-09-852-424-96	Sequence 96, App1
42	156	89.1	31 9 US-09-852-424-80	Sequence 80, App1
43	156	89.1	33 9 US-09-835-107-16	Sequence 16, App1
44	156	89.1	33 9 US-09-835-107-18	Sequence 18, App1
45	156	89.1	33 14 US-10-086-177A-16	Sequence 16, App1

## ALIGNMENTS

RESULT 1  
US-09-835-107-13  
Sequence 13, Application US/09835107  
Patent No. US20020165123A1  
GENERAL INFORMATION:  
APPLICANT: Tudan, Christopher R.  
APPLICANT: Mezouk, Ahmed  
APPLICANT: Arab, Lakhdar  
APPLICANT: Saxena, Geeta  
APPLICANT: Eaves, Connie J.  
APPLICANT: Cashman, Johanne  
APPLICANT: Clark-Lewis  
APPLICANT: Salati, Hassan  
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: SMAR012  
CURRENT APPLICATION NUMBER: US/09/835,107  
CURRENT FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: CA 2,305,036  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: US 60/232,425  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: CA 2,335,109  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: Patentm Ver. 2.0  
SEQ ID NO 13  
LENGTH: 31  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
NAME/KEY: DOMAIN  
LOCATION: (16..19)  
OTHER INFORMATION: spacer monomers (such as the illustrated glycine  
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3  
OTHER INFORMATION: or 4 glycines.  
OTHER INFORMATION: Synthesised in Laboratory:

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- OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) acid: or CTCB0013
US-09-835-107-13

Query Match          100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
DB 1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31

RESULT 2
US-09-835-107-15
; Sequence 15, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Baves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (15)..(18)
; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
; OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
; OTHER INFORMATION: or 4 glycines.
; OTHER INFORMATION: Synthesised in Laboratory:
; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) amide: or CTCB0017
; NAME/KEY: MOD RES
; LOCATION: (31)
; OTHER INFORMATION: AMIDATION
; US-09-835-107-15

Query Match          100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
DB 1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31

RESULT 3
US-09-835-107-20
; Sequence 20, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Baves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (15)..(18)
; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
; OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
; OTHER INFORMATION: or 4 glycines.
; OTHER INFORMATION: Synthesised in Laboratory:
; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) -E24/K28-cyclic acid
; US-09-835-107-20

Query Match          100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
DB 1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31

RESULT 4
US-09-835-107-21
; Sequence 21, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Baves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (15)..(18)
; OTHER INFORMATION: Cyclized, for example glutamate (R) and lysine (K)
; OTHER INFORMATION: residues may be joined by side chain cyclization
; OTHER INFORMATION: using a lactam formation procedure.
; OTHER INFORMATION: Synthesised in Laboratory:
; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) -E24/K28-cyclic acid
; US-09-835-107-21
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; NAME/KEY: DOMAIN
; LOCATION: (15)..(18)
; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
; OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
; OTHER INFORMATION: or 4 glycines.
; NAME/KEY: DOMAIN
; LOCATION: (20)..(24)
; OTHER INFORMATION: Cyclized, for example glutamate (E) and lysine (K)
; OTHER INFORMATION: residues may be joined by side chain cyclization
; OTHER INFORMATION: using a lactam formation.
; OTHER INFORMATION: Synthesised in laboratory.
; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/B24-cyclic acid
US-09-835-107-21

Query Match          100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
DB      1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31

RESULT 5
US-09-835-107-22
; Sequence 22, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Baves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DOMAIN
LOCATION: (24)..(28)
OTHER INFORMATION: Cyclized, for example (E) and lysine (K) residues
OTHER INFORMATION: may be joined by side chain cyclization using a
OTHER INFORMATION: lactam formation procedure.
OTHER INFORMATION: Synthesised in laboratory.
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-B24/K28-cyclic
NAME/KEY: MOD_RES
LOCATION: (31)
OTHER INFORMATION: amidation
US-09-835-107-22

Query Match          100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
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Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
DB      1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31

RESULT 6
US-09-835-107-23
; Sequence 23, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Baves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DOMAIN
LOCATION: (20)..(24)
OTHER INFORMATION: Cyclized, for example glutamate (E) and lysine
OTHER INFORMATION: (K) residues may be joined by side chain
OTHER INFORMATION: cyclization using a lactam formation procedure.
OTHER INFORMATION: Synthesised in laboratory.
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/B24-cyclic
NAME/KEY: MOD_RES
LOCATION: (31)
OTHER INFORMATION: amidation
US-09-835-107-23

Query Match          100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
DB      1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31

RESULT 7
US-09-835-107-26
; Sequence 26, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
```

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/ APPLICANT: Raves, Connie J.
/ APPLICANT: Cashman, Johanne
/ APPLICANT: Clark-Lewis
/ APPLICANT: Salari, Hassan
/ TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
/ FILE REFERENCE: SMAR012
/ CURRENT APPLICATION NUMBER: US/09/835,107
/ PRIOR FILING DATE: 2001-08-20
/ PRIOR APPLICATION NUMBER: CA 2,305,036
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: US 60/232,425
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: CA 2,335,109
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 26
/ LENGTH: 31
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: DOMAIN
/ LOCATION: (15)..(18)
/ OTHER INFORMATION: spacer monomers (such as the illustrated glycine
/ OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
/ OTHER INFORMATION: or 4 glycines.
/ NAME/KEY: DISULFID
/ LOCATION: (9)..(11)
/ OTHER INFORMATION: cysteine residues may for example be involved in
/ OTHER INFORMATION: bridge formation
/ OTHER INFORMATION: Synthesized in Laboratory:
/ OTHER INFORMATION: SDF-1(1-14) - (G)4-SDF-1(55-67) -C9/C11-cyclic acid
US-09-835-107-26

Query Match          100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No.2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
Db      1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31

RESULT 8
US-09-835-107-27
/ Sequence 27, Application US/09835107
/ Patent No. US20020165123A1
/ GENERAL INFORMATION:
/ APPLICANT: Tudan, Christopher R.
/ APPLICANT: Merzouk, Ahmed
/ APPLICANT: Arab, Lakhdar
/ APPLICANT: Saxena, Geeta
/ APPLICANT: Raves, Connie J.
/ APPLICANT: Cashman, Johanne
/ APPLICANT: Clark-Lewis
/ APPLICANT: Salari, Hassan
/ TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
/ FILE REFERENCE: SMAR012
/ CURRENT APPLICATION NUMBER: US/09/835,107
/ CURRENT FILING DATE: 2001-08-20
/ PRIOR APPLICATION NUMBER: CA 2,305,036
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: US 60/232,425
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: CA 2,335,109
/ PRIOR FILING DATE: 2001-02-23
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 27
/ LENGTH: 31
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
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/ NAME/KEY: DOMAIN
/ LOCATION: (15)..(18)
/ OTHER INFORMATION: spacer monomers (such as the illustrated glycine
/ OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
/ OTHER INFORMATION: or 4 glycines.
/ NAME/KEY: DISULFID
/ LOCATION: (9)..(11)
/ OTHER INFORMATION: Cysteine residues may for example be involved in
/ OTHER INFORMATION: bridge formation.
/ OTHER INFORMATION: Synthesized in Laboratory:
/ OTHER INFORMATION: SDF-1(1-14) - (G)4-SDF-1(55-67) -C9/C11-cyclic amide
/ NAME/KEY: MOD RES
/ LOCATION: (31)
/ OTHER INFORMATION: AMIDATION
US-09-835-107-27

Query Match          100.0%; Score 175; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No.2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
Db      1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31

RESULT 9
US-10-086-177A-13
/ Sequence 13, Application US/10086177A
/ Publication No. US20030148940A1
/ GENERAL INFORMATION:
/ APPLICANT: Tudan, Christopher R.
/ APPLICANT: Merzouk, Ahmed
/ APPLICANT: Saxena, Geeta
/ APPLICANT: Raves, Connie J.
/ APPLICANT: Cashman, Johanne
/ APPLICANT: Clark-Lewis, Ian
/ APPLICANT: Salari, Hassan
/ TITLE OF INVENTION: CXCR4 Agonist Treatment of Hematopoietic
/ TITLE OF INVENTION: Cells
/ FILE REFERENCE: SMAR-012CIP
/ CURRENT APPLICATION NUMBER: US/10/086,177A
/ CURRENT FILING DATE: 2002-02-26
/ PRIOR APPLICATION NUMBER: 09/835,107
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/232,425
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: CA 2,305,036
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: CA 2,335,109
/ PRIOR FILING DATE: 2001-02-23
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13
/ LENGTH: 31
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
/ OTHER INFORMATION: 3-SDF-1 (55-67) acid; or CTCBE0013
US-10-086-177A-13

Query Match          100.0%; Score 175; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No.2.5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
Db      1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31

RESULT 10
US-10-086-177A-15
/ Sequence 15, Application US/10086177A
```

```
Publication No. US20030148940A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Saxena, Geeta
APPLICANT: Baves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
FILE REFERENCE: SMAR-012CIP
CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
US-10-086-177A-15
```

```
Query Match      100.0%; Score 175; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 2,5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KPVSLSTYRCPCRFPGGGGLKMWIOYLEKALN 31
DB      1 KPVSLSTYRCPCRFPGGGGLKMWIOYLEKALN 31
```

```
RESULT 11
US-10-086-177A-20
Sequence 20, Application US/10086177A
Publication No. US20030148940A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Saxena, Geeta
APPLICANT: Baves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
FILE REFERENCE: SMAR-012CIP
CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
```

```
FEATURE:
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
OTHER INFORMATION: 4-SDF-1 (55-67) - E24/K28-cyclic acid
US-10-086-177A-20
```

```
Query Match      100.0%; Score 175; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 2,5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KPVSLSTYRCPCRFPGGGGLKMWIOYLEKALN 31
DB      1 KPVSLSTYRCPCRFPGGGGLKMWIOYLEKALN 31
```

```
RESULT 12
US-10-086-177A-21
Sequence 21, Application US/10086177A
Publication No. US20030148940A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Saxena, Geeta
APPLICANT: Baves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
FILE REFERENCE: SMAR-012CIP
CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
US-10-086-177A-21
```

```
Query Match      100.0%; Score 175; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 2,5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KPVSLSTYRCPCRFPGGGGLKMWIOYLEKALN 31
DB      1 KPVSLSTYRCPCRFPGGGGLKMWIOYLEKALN 31
```

```
RESULT 13
US-10-086-177A-22
Sequence 22, Application US/10086177A
Publication No. US20030148940A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Saxena, Geeta
APPLICANT: Baves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
FILE REFERENCE: SMAR-012CIP
CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
```

```
/ FILE REFERENCE: SMAR-012CIP
/ CURRENT APPLICATION NUMBER: US/10/086,177A
/ CURRENT FILING DATE: 2002-02-26
/ PRIOR APPLICATION NUMBER: 09/835,107
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/232,425
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: CA 2,305,036
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: CA 2,335,109
/ PRIOR FILING DATE: 2001-02-23
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 22
/ LENGTH: 31
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
/ OTHER INFORMATION: 4-SDF-1 (55-67) - E24/K28-cyclic acid: or CTCG0022
US-10-086-177A-22
```

```
Query Match          100.0%; Score 175; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 2,5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
Db 1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
```

```
RESULT 14
US-10-086-177A-23
/ Sequence 23, Application US/10086177A
/ Publication No. US20030148940A1
/ GENERAL INFORMATION:
/ APPLICANT: Tudan, Christopher R.
/ APPLICANT: Merzouk, Ahmed
/ APPLICANT: Saxena, Geeta
/ APPLICANT: Eaves, Connie J.
/ APPLICANT: Cashman, Johanne
/ APPLICANT: Clark-Lewis, Ian
/ APPLICANT: Salari, Hassan
/ TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
/ FILE REFERENCE: SMAR-012CIP
/ CURRENT APPLICATION NUMBER: US/10/086,177A
/ CURRENT FILING DATE: 2002-02-26
/ PRIOR APPLICATION NUMBER: 09/835,107
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/232,425
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: CA 2,305,036
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: CA 2,335,109
/ PRIOR FILING DATE: 2001-02-23
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 23
/ LENGTH: 31
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
/ OTHER INFORMATION: 4-SDF-1 (55-67) - K20/E24-cyclic acid: or CTCG0021
US-10-086-177A-23
```

```
Query Match          100.0%; Score 175; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 2,5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
Db 1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
```

```
Db 1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
```

```
RESULT 15
US-10-086-177A-26
/ Sequence 26, Application US/10086177A
/ Publication No. US20030148940A1
/ GENERAL INFORMATION:
/ APPLICANT: Tudan, Christopher R.
/ APPLICANT: Merzouk, Ahmed
/ APPLICANT: Saxena, Geeta
/ APPLICANT: Eaves, Connie J.
/ APPLICANT: Cashman, Johanne
/ APPLICANT: Clark-Lewis, Ian
/ APPLICANT: Salari, Hassan
/ TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
/ FILE REFERENCE: SMAR-012CIP
/ CURRENT APPLICATION NUMBER: US/10/086,177A
/ CURRENT FILING DATE: 2002-02-26
/ PRIOR APPLICATION NUMBER: 09/835,107
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/232,425
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: CA 2,305,036
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: CA 2,335,109
/ PRIOR FILING DATE: 2001-02-23
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 26
/ LENGTH: 31
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
/ OTHER INFORMATION: 4-SDF-1 (55-67) - C9/C11-cyclic acid
US-10-086-177A-26
```

```
Query Match          100.0%; Score 175; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 2,5e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
Db 1 KPVSLSYRCPCRFPGGGGLKMIQIYLEKALN 31
```

```
Search completed: January 4, 2005, 16:05:00
Job time : 102.131 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 15:43:59 ; Search time 12.7049 Seconds  
(without alignments)  
234.769 Million cell updates/sec

Title: US-10-086-177A-13

Perfect score: 175  
Sequence: 1 KPVSLSTRCPFRFFGGGLKMWIKYLEKALN 31

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	66.9	89	2	I53416 Interleukin-8 Homo
2	117	66.9	89	2	A53497 pre-B-cell growth-
3	117	66.9	93	2	G01540 cytokine SDF-1-bet
4	117	66.9	93	2	I81182 cytokine - mouse
5	61	34.9	1084	2	T08583 cellulose synthase
6	61	34.9	1088	2	H84604 probable cellulose
7	60.5	34.6	974	2	T10797 cellulose synthase
8	58	33.1	469	2	C83345 probable class III
9	58	33.1	1081	2	T52028 cellulose synthase
10	56	32.0	233	2	T35594 hypothetical prote
11	54	30.9	398	2	T52311 isopenicillin N ep
12	53	30.3	454	2	C64104 gamma-aminobutyric
13	53	30.3	470	2	T46814 gamma-aminobutyric
14	53	30.3	470	2	B95419 diaminobutyrate-py
15	50	28.6	202	2	A13489 cytochrome c-552 [
16	50	28.6	588	2	S34786 catechol oxidase (
17	50	28.6	685	2	T10800 cellulose synthase
18	49.5	28.3	170	2	B85359 hypothetical prote
19	49.5	28.3	577	2	I50731 Ig heavy chain - n
20	49	28.0	386	2	C81419 probable type IIS
21	49	28.0	508	2	F87198 glycerol kinase [i
22	49	28.0	517	2	A70793 probable glycerol
23	49	28.0	556	1	A53376 tryptophan 2-mono
24	49	28.0	557	1	A25493 tryptophan 2-mono
25	49	28.0	1722	2	A88470 protein C28H8.3 [i
26	48	27.4	189	2	D69389 DNA-directed RNA p
27	48	27.4	309	1	S34198 IGF PC receptor II
28	48	27.4	331	1	LNMSER IGF PC receptor. 1
29	48	27.4	383	2	C90136 26S proteasome SU

30	48	27.4	593	2	S30958 gene 13 protein -
31	48	27.4	661	2	S45131 probable membrane
32	48	27.4	1016	2	F82159 transporter, Acrb/
33	48	27.4	1429	2	S06434 homeotic protein 1
34	47.5	27.1	439	2	E32298 hypothetical prote
35	47.5	27.1	722	2	H96986 endo-1,4-beta gluc
36	47	26.9	203	2	I50481 synapse protein SN
37	47	26.9	398	2	S30901 isopenicillin N ep
38	47	26.9	409	2	S01825 transforming growt
39	47	26.9	623	2	T40685 phosphatidylcholin
40	47	26.9	1108	2	T35827 probable membrane
41	47	26.9	1400	2	T22644 hypothetical prote
42	46.5	26.6	1112	2	D96753 similar to disease
43	46.5	26.6	1287	2	T22235 hypothetical prote
44	46	26.3	122	2	T45165 succinate dehydrog
45	46	26.3	212	2	S73466 probable DNA prima

## ALIGNMENTS

```

RESULT 1
I53416
Interleukin-8 homolog - mouse
C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I53416
R:Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.
Exp. Cell Res. 215, 284-293, 1994
A:Title: Molecular cloning of TP41, a gene whose expression is repressed by the tumor
A:Reference number: I53416, MUID:95073497, PMID:7982471
A:Accession: I53416
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89 <R85>
A:Cross-references: GB:S74318; NID:G786393; PIDN:AA82650.1; PID:G786394
C:Genetic:
A:Gene: TP41
C:Superfamily: beta-thromboglobulin

Query Match      66.9%; Score 117; DB 2; Length 89;
Best Local Similarity 40.3%; Pred. No. 5.4e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY      1 KPVSLSTRCPFRFFGG-----GGLKMWIK 24
Db      22 KPVSLSTRCPFRFFSHIRANVGHILNTNPICALIVARLKNNNRQCIDPILKMWIK 81
QY      25 YLEKALN 31
Db      82 YLEKALN 88

RESULT 2
A53497
pre-B-cell growth-stimulating factor precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004
C:Accession: A53497; I59582
R:Nagasawa, T.; Kikutani, H.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994
A:Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.
A:Reference number: A53497; MUID:94181581; PMID:8134392
A:Accession: A53497
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-89 <NAG>
A:Cross-references: UNIPROT:P40224; GB:D21072; NID:G413905; PIDN:BA04648.1; PID:G466845
R:Tahtiro, K.; Tada, H.; Heliker, R.; Shiroyu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I memb
A:Reference number: I59582; MUID:93342488; PMID:8342023
A:Accession: I59582

```

A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-89 <RES>  
A/Cross-references: GB:LI2029, NID:g393179, PIDN:AAA40100.1, PID:g393180  
C/Genetics:  
A:Gene: SDF-1-alpha  
C/Superfamily: beta-chromoglobulin  
C/Keywords: cytokine

Query Match 66.9%; Score 117; DB 2; Length 89;  
Best Local Similarity 40.3%; Pred. No. 5.4e-09;  
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GGLKXIOE 24  
DB 22 KPVSLSYRCPCRFESHARANYKHLKILNTPNCALQIVARLKNNNRQVCIDPKLXIOE 81  
QY 25 YLEKALN 31  
DB 82 YLEKALN 88

RESULT 3  
G01540  
Cytokine SDF-1-beta - human  
C/Species: Homo sapiens (man)  
C/Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 09-Jul-2004  
C/Accession: G01540  
R/Spotila, L.D.  
Submitted to the EMBL Data Library, October 1994  
A/Reference number: G07697  
A/Accession: G01540  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-93 <SPO>  
A/Cross-references: UNIPROT:P48061, EMBL:U16752, NID:g1272194, PID:G571508  
C/Superfamily: beta-chromoglobulin

Query Match 66.9%; Score 117; DB 2; Length 93;  
Best Local Similarity 40.3%; Pred. No. 5.7e-09;  
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GGLKXIOE 24  
DB 22 KPVSLSYRCPCRFESHARANYKHLKILNTPNCALQIVARLKNNNRQVCIDPKLXIOE 81  
QY 25 YLEKALN 31  
DB 82 YLEKALN 88

RESULT 4  
I81182  
Cytokine - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C/Accession: I81182  
R/Tashiro, K.; Tada, H.; Heller, R.; Shirozu, M.; Nakano, T.; Honjo, T.  
Science 261, 600-603, 1993  
A/Title: Signal sequence trap: a cloning strategy for secreted proteins and type I membr  
A/Reference number: I59582; MUID:93342488; PMID:8342023  
A/Accession: I81182  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-93 <RES>  
A/Cross-references: UNIPROT:P40224; GB:LI2030, NID:g393181, PIDN:AAA40101.1, PID:g393182  
C/Genetics:  
A:Gene: SDF-1-beta  
C/Superfamily: beta-chromoglobulin

Query Match 66.9%; Score 117; DB 2; Length 93;  
Best Local Similarity 40.3%; Pred. No. 5.7e-09;  
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GGLKXIOE 24  
DB 22 KPVSLSYRCPCRFESHARANYKHLKILNTPNCALQIVARLKNNNRQVCIDPKLXIOE 81  
QY 25 YLEKALN 31  
DB 82 YLEKALN 88

RESULT 5  
T08583  
Cellulose synthase (EC 2.4.1.-) catalytic chain - Arabidopsis thaliana

N/Alternate names: protein T22F8.250  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C/Accession: T08583; T09014  
R/Bevan, M.; Zimmermann, W.; Gruenleisen, A.; Wambutt, R.; Bancroft, I.; Newes, H.W.; Ma,  
submitted to the Protein Sequence Database, May 1999  
A/Reference number: Z16442  
A/Accession: T08583

A:Molecule type: DNA  
A:Residues: 1-1084 <BEV>  
A/Cross-references: UNIPROT:Q48947; EMBL:AL050351; GSPDB:GN00062; ATSP:T22F8.250  
A/Experimental source: cultivar Columbia; BAC clone T22F8  
R/Arifol, T.; Peng, L.; Betzner, A.S.; Burn, J.; Wiltke, W.; Herth, W.; Camilleri, C.;  
Science 279, 717-720, 1998  
A/Title: Molecular analysis of cellulose biosynthesis in Arabidopsis.  
A/Reference number: Z13745; MUID:9811412; PMID:9445479  
A/Accession: T09014  
A/Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1084 <ARI>  
A/Cross-references: EMBL:AR027173, NID:g2827140; PIDN:AA39335.1; PID:g2827141  
A/Experimental source: cultivar Columbia  
C/Genetics:  
A:Gene: ATSP:T22F8.250; Ath-A  
A/Map position: 4  
A/Intons: 27/3; 156/3; 191/1; 254/2; 343/2; 458/3; 504/3; 546/3; 617/3; 708/1; 773/3;  
C/Keywords: cell wall synthesis; glycosyltransferase; hexosyltransferase

Query Match 34.9%; Score 61; DB 2; Length 1084;  
Best Local Similarity 43.5%; Pred. No. 2.8;  
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 VSLSYRCPCRFPGGGLKXIOE 25  
DB 833 IFLSRHCPIWYGYGGGLKLERF 855

RESULT 6  
H84604  
Probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: H84604  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.F.; Bentol, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffett, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.  
euser, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter,  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: H84604  
A/Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1088 <STO>  
A/Cross-references: UNIPROT:Q9J22; GB:AE002093, NID:g4417271; PIDN:AAD20396.1; GSPDB:GT  
C/Genetics:  
A:Gene: At2G21770  
A/Map position: 2

Query Match 34.9%; Score 61; DB 2; Length 1088;  
Best Local Similarity 43.5%; Pred. No. 2.8;





## RESULT 12

C64104

gamma-aminobutyrate aminotransferase (EC 2.6.1.-) - Haemophilus influenzae (strain Rd K)

C/Species: Haemophilus influenzae

C/Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004

C/Accession: C64104; JCS879

R/Accession: R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kierlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodet, A.; Kelley, J.M.; Weidman, J.

D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A./Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A/Reference number: A64000; MUID:95350630; PMID:7542800

A/Accession: C64104

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-454 &lt;11GR&gt;

A/Cross-references: UNIPROT:P44951; GB:U52776; GB:I42023; NID:g1573969; PIDN:AAC22610.1;

R/ikai, H.; Yamamoto, S.

Bioi. Pharm. Bull. 21, 170-173, 1998

A/Title: Two genes involved in the 1,3-diaminopropane production pathway in Haemophilus

A/Reference number: JCS879; MUID:96173550; PMID:9514614

A/Accession: JCS879

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-454 &lt;11GR&gt;

A/Cross-references: GB:U52776; NID:g1573969; PIDN:AAC22610.1; PID:g1573974

C/Comment: This enzyme is involved in the pathway of 1,3-diaminopropane synthesis.

C/Genetics:

A/Note: neither the complete nucleic acid sequence nor the complete translation are show

C/Superfamily: beta-alanine-pyruvate transaminase

C/Keywords: aminotransferase; phosphoprotein; pyridoxal phosphate

F/287/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 30.3%; Score 53; DB 2; Length 454;

Best Local Similarity 38.5%; Pred. No. 16;

Matches 10; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

DB 2 PVSLSYRCPCRFPGGGG--LKMIQYIEKAL 27

DB 181 PYPHYRCPCFGEIGGAGAKAVEQYFE 206

## RESULT 13

T46814

gamma-aminobutyrate aminotransferase (EC 2.6.1.-) rhba [imported] - Rhizobium meliloti

C/Species: Rhizobium meliloti

C/Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 09-Jul-2004

C/Accession: T46814

R/Lynch, D.; O'Connell, M.; O'Brien, J.

submitted to the EMBL Data Library, December 1998

A/Description: Cloning and sequence analysis of the Sinorhizobium meliloti 2011 rhizobac

A/Reference number: Z24097

A/Accession: T46814

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-470 &lt;LTV&gt;

A/Cross-references: UNIPROT:Q923R2; EMBL:AF110737; PIDN:AAD09412.1

A/Experimental source: strain 2011

C/Genetics:

A/Gene: rhba

C/Function:

A/Pathway: siderophore biosynthesis

C/Superfamily: beta-alanine-pyruvate transaminase

C/Keywords: aminotransferase

Query Match 30.3%; Score 53; DB 2; Length 470;

Best Local Similarity 43.8%; Pred. No. 16;

Matches 14; Conservative 2; Mismatches 10; Indels 6; Gaps 2;

DB 2 PVSLSYRCPCRFPGGGG--LKMIQYIEKAL 30

DB 181 PYPHYRCPCFGEIGGAGAKAVEQYFE 206

DB 198 PYPAYRCPCFPGGGG--LKMIQYIEKAL 226

## RESULT 14

B95419

diaminobutyrate-pyruvate transaminase (EC 2.6.1.46) Rhba [imported] - Sinorhizobium meliloti

C/Species: Sinorhizobium meliloti

C/Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004

C/Accession: B95419

R/Barnett, M.T.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barlow-Hubler, F.; Bowers,

J.; Kalman, S.; Keating, D.H.; Palm, C.; Beck, M.C.; Surzycki, R.; Wells, D.H.; Yen, K.C.

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A/Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti

A/Reference number: A95262; MUID:21396509; PMID:1148132

A/Accession: B95419

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-470 &lt;KUR&gt;

A/Cross-references: UNIPROT:Q923R2; GB:AB06469; PIDN:AAK65916.1; PID:g14524429; GSPDB:G

R/Galibert, F.; Flinn, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barlow-Hubler,

Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpriel, N.A.; Fisher, R.F.,

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, E.; Komp, C.; Lelaure,

hehault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K

A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A/Reference number: A96039; MUID:21368234; PMID:11474104

A/Contents: annotation

C/Genetics:

A/Gene: rhba

A/Genome: plasmid

C/Superfamily: beta-alanine-pyruvate transaminase

C/Keywords: aminotransferase

Query Match 30.3%; Score 53; DB 2; Length 470;

Best Local Similarity 43.8%; Pred. No. 16;

Matches 14; Conservative 2; Mismatches 10; Indels 6; Gaps 2;

DB 2 PVSLSYRCPCRFPGGGG--LKMIQYIEKAL 30

DB 198 PYPAYRCPCFPGGGG--LKMIQYIEKAL 226

## RESULT 15

A13489

cytochrome c-552 [imported] - Brucella melitensis (strain 16M)

C/Species: Brucella melitensis

C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 15-Mar-2004

C/Accession: A13489

R/Delvecchio, V.G.; Kaputal, V.; Redkar, R.J.; Patra, G.; Mujter, C.; Los, T.; Ivanova,

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A/Reference number: AD3252; PMID:11756688

A/Accession: A13489

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-202 &lt;KUR&gt;

A/Cross-references: GB:AE008917; PIDN:AAL53084.1; PID:g17983947; GSPDB:GNO0190

A/Experimental source: strain 16M

C/Genetics:

A/Gene: BME1903

C/Function:

A/Pathway: membrane-bound c-type cytochrome; cytochrome c homology

C/Superfamily: cytochrome; heme; iron; metalloprotein

C/Keywords: cytochrome; heme; iron; metalloprotein

F/88/Binding site: heme iron (His) (axial ligand) #status predicted

F/153/Binding site: heme iron (Met) (axial ligand) #status predicted

Query Match 28.6%; Score 50; DB 2; Length 202;

Best Local Similarity 44.0%; Pred. No. 19;

Matches 11; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

DB 2 PVSLSYRCPCRFPGGGG--LKMIQYIEKAL 30

DB 198 PYPAYRCPCFPGGGG--LKMIQYIEKAL 226

Qy 6 SYRCPFRFGGGLKWIQETLEKAL 30  
Db 117 SYSAMKEFGAAGNKWDPEHLNKFL 141

Search completed: January 4, 2005, 15:44:33  
Job time : 13.7049 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: January 4, 2005, 15:43:59 ; Search time 59.459 Seconds  
(without alignments)  
299.982 Million cell updates/sec

Title: US-10-086-177A-13  
Perfect score: 175  
Sequence: 1 KPVSLSYRCRCRFRGGGLKRWIKRYLEKALN 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	66.9	89	1	SDP1_MOUSE
2	117	66.9	89	2	Q8H7FO
3	117	66.9	89	2	BAA28601
4	117	66.9	89	2	CAC10203
5	117	66.9	89	2	BAC32216
6	117	66.9	89	2	BAC35845
7	117	66.9	89	2	CAG29279
8	117	66.9	92	2	Q9H554
9	117	66.9	93	1	SDP1_FELCA
10	117	66.9	93	1	SDP1_HUMAN
11	117	66.9	116	2	Q6EKW4
12	117	66.9	137	2	Q80ZM4
13	116	66.3	89	2	Q6T7C0
14	116	66.3	89	2	AAR88102
15	116	66.3	89	2	AAR91695
16	116	66.3	131	2	Q6T7B9
17	116	66.3	131	2	AAR91696
18	114	65.1	89	2	Q9QZD1
19	114	65.1	119	2	Q80YV8
20	105	60.0	94	2	Q8UUY9
21	105	60.0	94	2	AAR61945
22	61	34.9	507	2	Q93YF8
23	61	34.9	1088	2	Q9S7J2
24	61	34.9	1088	2	Q9S7J2
25	60.5	34.6	974	2	Q9M1N0
26	60.5	34.6	974	2	Q9M1N0
27	60	34.3	1078	2	Q6UDF1
28	60	34.3	1078	2	AAR23310
29	59	33.7	1084	2	Q6GUG6
30	58	33.1	346	2	Q8L778
31	58	33.1	366	2	Q94JG6

32	58	33.1	460	2	Q6D4Z7	Q6D4Z7 erwinia car
33	58	33.1	469	2	Q9T168	Q9T168 pseudomonas
34	58	33.1	1069	2	Q9F1B9	Q9F1B9 arabidopsis
35	58	33.1	1081	2	Q6S338	Q6S338 arabidopsis
36	58	33.1	1084	2	Q9F6F9	Q9F6F9 arabidopsis
37	58	33.1	1087	2	Q6XZC2	Q6XZC2 populus tre
38	58	33.1	1087	2	AAP40636	AAP40636 populus t
39	57.5	32.9	939	2	Q943H3	Q943H3 cryza sativ
40	57	32.6	192	2	Q707H1	Q707H1 escherichia
41	57	32.6	192	2	CAE85184	CAE85184 escherich
42	57	32.6	199	2	Q7C009	Q7C009 shigella fl
43	57	32.6	199	2	Q83J00	Q83J00 shigella fl
44	57	32.6	199	2	Q8FRT6	Q8FRT6 escherichia
45	57	32.6	424	2	Q9VCS4	Q9VCS4 dtrosophila

## ALIGNMENTS

RESULT 1	ID	SDP1_MOUSE	STANDARD;	PRT;	89 AA.
AC	P40224;				
DT	01-FEB-1995 (Rel. 31, Last sequence update)				
DT	01-FEB-1995 (Rel. 31, Last sequence update)				
DT	01-OCT-2004 (Rel. 45, Last annotation update)				
DE	Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell growth stimulating factor) (PBSF) (12-O-tetradecanoylphorbol 13-acetate repressed protein 1) (TPAR1) (Thymic lymphoma cell stimulating factor) (Tlspf).				
DE	factor) (Tlspf).				
GN	Name=CXCL12; Synonyms=Sdf1;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI	TaxID=10090;				
RM	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=94181581; PubMed=8134392;				
RA	Nagasawa T., Kikuchi H., Kishimoto T.,				
RT	Molecular cloning and structure of a pre-B-cell growth-stimulating factor."				
RL	Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309(1994).				
RM	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93342488; PubMed=8342023;				
RA	Taahiro K., Tada H., Heilker R., Shirozu M., Nakano T., Honjo T.,				
RT	"Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins."				
RL	Science 261:600-603(1993).				
RM	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=95073497; PubMed=7982471;				
RA	Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D., Weinstein I.B.,				
RT	"Molecular cloning of TPRI, a gene whose expression is repressed by the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA)."				
RL	Exp. Cell Res. 215:284-293(1994).				
RM	[4]				
RP	SEQUENCE FROM N.A.				
RX	STRAIN=AKR/J;				
RA	Nomura M., Nakata Y., Uzawa A., Nose M., Akashi M., Suzuki G.,				
RT	Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.				
RM	[5]				
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).				
RX	STRAIN=C57BL/6J; TISSUE=Kidney;				
RA	MEDLINE=22354683; PubMed=1246851; DOI=10.1038/nature01266;				
RT	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,				
RL	Nakada I., Osato N., Saito R., Suzuki H., Yamanka I., Kiyosawa H.,				
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,				
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,				
RA	Schirral L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,				
RA	Blake J.A., Bradt D., Brusci V., Choitha C., Coriani L.E., Cousins S.,				
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,				
RA	Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,				

RA Grimmond J., Gueffroy S., Hirokawa N., Jackson I. J., Jarvis E.D.,  
RA Kamei A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kutrichkin I.V., Lee Y., Lenhard B., Lyon P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Nunata K., Okido T., Pavan W.J., Petrea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Saldelli A., Schneider C., Sempke C.A., Seou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Waltered C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wyshew-Borle A., Yanagisawa M., Yang I., Yang L.,  
RA Yuen Z., Zavolan M., Zhu Y., Zimmer A., Carroll P., Hayatsu N.,  
RA Hirokawa-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
RA Shitara T., Waki K., Kawai K., Atawa K., Atakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yamashita A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
[6]  
RP SEQUENCE FROM N.A. (ISOFROM ALPHA).  
RC STRAIN=CS7BL/6J; TISSUE=Mammary gland;  
RC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RX STRAUBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datschenko L., Marutani K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carlini P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Farley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,  
RA Schenker A., Schin J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: Chemoattractant active on T-lymphocytes, monocytes, but  
CC not neutrophils.  
CC -1- FUNCTION: Stimulates the proliferation of bone marrow-derived b  
CC progenitor cells in the presence of IL-7 as well as growth of the  
CC stromal cell-dependent B-cell clone DM34 cells.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named Isoforms=2;  
CC Name=Alpha;  
CC Isoid=P40224-1; Sequence=Displayed;  
CC Name=Beta;  
CC Isoid=P40224-1; Sequence=Displayed;  
CC -1- SIMILARITY: Belongs to the interleukin alpha (chemokine CXCL)  
CC family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation at  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/annouce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC -----  
DR EMBL; D21072; BAA04648.1; -  
DR EMBL; L12029; AAA40100.1; -  
DR EMBL; L12030; AAA40101.1; -  
DR EMBL; S74318; AAB32650.1; -  
DR EMBL; D43804; BAA07862.1; -

Query Match	Similarity	Score	DB 1	Length	DB 2	Length	DB 3	Length
EMBL: D43805; BAA07863.1; -	66.9%	117	DB 1	89				
EMBL: AK075596; BAC35945.1; -	66.9%	117	DB 1	89				
EMBL: BC006640; AA006640.1; -	66.9%	117	DB 1	89				
PIR: A53497; A53497.	66.9%	117	DB 1	89				
PIR: I81182; I81182.	66.9%	117	DB 1	89				
HSSP: P48061; 1SDP.	66.9%	117	DB 1	89				
MGI: 103556; Cxcl12.	66.9%	117	DB 1	89				
GO: 0008009; F:chemokine activity; IDA.	66.9%	117	DB 1	89				
GO: 0007420; P:brain development; IDA.	66.9%	117	DB 1	89				
GO: 0030334; P:regulation of cell migration; IDA.	66.9%	117	DB 1	89				
GO: 0042098; P:T-cell proliferation; IMP.	66.9%	117	DB 1	89				
InterPro: IPR002473; C-X-C/Interlkn_8.	66.9%	117	DB 1	89				
InterPro: IPR001811; Chemokine_116.	66.9%	117	DB 1	89				
InterPro: IPR001089; CXCL12; C-X-C/Interlkn_8.	66.9%	117	DB 1	89				
Pfam: PF00048; IL8; 1.	66.9%	117	DB 1	89				
PRINTS: PR00436; INTERLEUKIN.	66.9%	117	DB 1	89				
PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.	66.9%	117	DB 1	89				
Alternative splicing; Chemotaxis; Cytokine; Growth factor; Signal.	66.9%	117	DB 1	89				
SIGNAL	66.9%	117	DB 1	89				
CHAIN	66.9%	117	DB 1	89				
DISULFID	66.9%	117	DB 1	89				
DISULFID	66.9%	117	DB 1	89				
VASAPLIC	66.9%	117	DB 1	89				
SEQUENCE	66.9%	117	DB 1	89				
Query Match	Similarity	Score	DB 1	Length	DB 2	Length	DB 3	Length
Best Local	Similarity	Score	DB 1	Length	DB 2	Length	DB 3	Length
Matches	Conservative	0	Mismatches	4	Indels	36	Gaps	1



```

RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RA Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK045092; BAC32216.1; -.
SQ SEQUENCE 89 AA; 10032 MW; C4B8AD69078E55FA CRC64;

Query Match 66.9%; Score 117; DB 2; Length 89;
Best local Similarity 40.3%; Pred. No. 6e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKXIQE 24
    |||||
DB 22 KPVSLSYRCPCRFESHARANYKHLKILNTPNCALQIVARLKNNNRQVCIDPKLXIQE 81
    |||||
QY 25 YLEKALN 31
    |||||
DB 82 YLEKALN 88

RESULT 6
BAC35845 PRELIMINARY; PRT; 89 AA.
AC BAC35845;
DT 14-APR-2004 (TREMBLrel. 27, Created)
DT 14-APR-2004 (TREMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)
DE Adult male kidney cDNA, RIKEN full-length enriched library,
DE clone:0610039H13 product:stromal cell derived factor 1, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN PANTOM Consortium;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690 (2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning."
RL Mech. Enzymol. 303:19-44 (1999).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

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RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1671-1630 (2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Saito R., Akiyama U., Nishi K., Kitesuna T., Tashiro H., Itoh M.,
RA Smit N., Ishii Y., Nakamura S., Hazama M., Nishihara T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujimoto S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multichannel sequencer."
RL Genome Res. 10:1757-1771 (2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA Adachi U., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Bono H., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito R., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamuro T., Yamana K., Yasunishi A.,
RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.,
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075596; BAC35845.1; -.
SQ SEQUENCE 89 AA; 10032 MW; C4B8AD69078E55FA CRC64;

Query Match 66.9%; Score 117; DB 2; Length 89;
Best local Similarity 40.3%; Pred. No. 6e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKXIQE 24
    |||||
DB 22 KPVSLSYRCPCRFESHARANYKHLKILNTPNCALQIVARLKNNNRQVCIDPKLXIQE 81
    |||||
QY 25 YLEKALN 31
    |||||
DB 82 YLEKALN 88

RESULT 7
CAG329279 PRELIMINARY; PRT; 89 AA.
AC CAG329279;
DT 20-MAY-2004 (TREMBLrel. 27, Created)
DT 20-MAY-2004 (TREMBLrel. 27, Last sequence update)
DT 20-MAY-2004 (TREMBLrel. 27, Last annotation update)
DE CKLI12 protein (Fragment).
GN CKLI12.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA Ebert U., Schick W., Neubert P., Schatten R., Henze S., Korn B.,
RT "Cloning of human full open reading frames in Gateway (TM) system entry
RT vector (pDONR201)."
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR450283; CAG329279.1; -.
FT NON TER 89
SQ SEQUENCE 89 AA; 10103 MW; 62B44E8D209C3A14 CRC64;

Query Match 66.9%; Score 117; DB 2; Length 89;

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Best Local Similarity 40.3%; Pred. No. 6e-09; Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GGKWKIOE 24  
DB 22 KPVSLSYRCPCRFESHVAVANVHKLITNPNCALQIVARLKNNNROVCIDPKLWKIOE 81

QY 25 YLEKALN 31  
DB 82 YLEKALN 88

## RESULT 8

Q9H554 PRELIMINARY; PRT; 92 AA.

AC Q9H554;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE BA20J15.1.2 (Stromal cell-derived factor 1, isoform beta)  
DE (Fragment).  
GN Name=SDFL;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
CX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Blvd C.;  
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AL137026; CAC10202.1; -  
DR HSSP; P48061; ISDF.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0008009; F:chemokine activity; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR002473; C-X-C/Interlkn\_8.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR PRINTS; PR00436; INTERLEUKIN8.  
DR SMART; SM00199; SCY; 1.  
FT NON TER  
SQ SEQUENCE 92 AA; 10510 MW; AEF0CA02B44BBD20 CRC64;

Query Match 66.9%; Score 117; DB 2; Length 92;  
Best Local Similarity 40.3%; Pred. No. 6.2e-09;  
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GGKWKIOE 24  
DB 22 KPVSLSYRCPCRFESHVAVANVHKLITNPNCALQIVARLKNNNROVCIDPKLWKIOE 81

QY 25 YLEKALN 31  
DB 82 YLEKALN 88

## RESULT 9

SDFL FELCA STANDARD; PRT; 93 AA.

AC Q62657;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).  
GN Name=CXCL12; Synonyms=SDFL;  
DE Feline interleukin cactus (Cat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Placentalia; Felidae; Felis.  
CX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
RC TISSUE=Thymus;  
MEDLINE=98450506; PubMed=9777331;

RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K.,  
RA Cai J.S., Sato E., Kohmoto M., Mikami T.;  
RT "Molecular cloning and sequencing of feline stromal cell-derived  
RT factor-1 alpha and beta."  
RL Eur. J. Immunogenet. 25:303-305(1998).  
CC -1- FUNCTION: Chemottractant active on T-lymphocytes, monocytes, but  
CC not neutrophils.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Beta;  
CC Name=Alpha;  
CC IsoId=O62657-1; Sequence=Displayed;  
CC IsoId=O62657-2; Sequence=VSP\_001055;  
CC -1- SIMILARITY: Belongs to the Interleukin alpha (chemokine Cxc)  
CC family.

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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

DR EMBL; AB011966; BA28602.1; -  
DR HSSP; P48061; ISDF.  
DR InterPro; IPR002473; C-X-C/Interlkn\_8.  
DR InterPro; IPR001811; Chemokine IL8.  
DR InterPro; IPR001089; CXC\_chemokine\_small.  
DR Pfam; PF00048; IL8; 1.  
DR PRINTS; PR00436; INTERLEUKIN8.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00471; SMALL\_CYTOKINES\_CXC; FALSE NEG.  
KW Alternative splicing; Chemotaxis; Cytokine; Growth factor; Signal.  
FT SIGNAL 1 21  
FT CHAIN 22 93  
FT DISULFID 30 55  
FT DISULFID 32 71  
FT VARSPDIC 90 93  
FT FT  
SQ SEQUENCE 93 AA; 10581 MW; 44FC763711B9BE37 CRC64;

Query Match 66.9%; Score 117; DB 1; Length 93;  
Best Local Similarity 40.3%; Pred. No. 6.3e-09;  
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GGKWKIOE 24  
DB 22 KPVSLSYRCPCRFESHVAVANVHKLITNPNCALQIVARLKNNNROVCIDPKLWKIOE 81

QY 25 YLEKALN 31  
DB 82 YLEKALN 88

## RESULT 10

SDFL HUMAN STANDARD; PRT; 93 AA.

AC P48061;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (pre-B cell  
DE growth stimulating factor) (PBSF) (HIRH) (Contains: SDF-1-beta(3-72);  
DE SDF-1-alpha(3-67)).  
GN Name=CXCL12; Synonyms=SDFL;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
CX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Spocchia L.D.;  
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9603262; PubMed=7490086;  
 RA Shitrou M., Nakano T., Inazawa J., Tashiro K., Tada H., Shinohara T.,  
 RT Honjo T.;  
 RL "Structure and chromosomal localization of the human stromal cell-  
 derived factor 1 (SDF1) gene.";  
 RL Genomics 28:495-500(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
 RC TISSUE=Liver;  
 RA Begum N.A., Barnard G.F.;  
 RT "Nucleotide sequence of hHRH, human interleukin reduced in hepatomas.";  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15164054; DOI=10.1038/nature02462;  
 RA Deloukas P., Barthrowl M.E., Grahm D.V., Rubinfeld M., French L.,  
 RA Steward C.A., Sims S.K., Jones M.C., Searle S., Scott C., Howe K.,  
 RA Hunt S.E., Andrews T.D., Gilbert J.G.R., Swardbeck D., Ashurst J.L.,  
 RA Taylor A., Batties J., Bird C.P., Alencough R., Almeida J.P.,  
 RA Ashwell R.I.S., Ambrose K.D., Babbage A.K., Bagguley C.D., Bailey J.,  
 RA Banerjee R., Bates K., Beasley H., Bray-Allen S., Brown A.J.,  
 RA Brown J.V., Burford D.C., Burfell W., Burton J., Cahill P., Cantre D.,  
 RA Carter N.P., Chapman J.C., Clark S.Y., Clarke G., Clee C.M., Clegg S.,  
 RA Corby N., Coulson A., Dhani P., Dutta I., Dunn M., Faulkner L.,  
 RA Frankish A., Frankland J.A., Garner P., Garnett J., Griddle S.,  
 RA Griffiths C., Grocock R., Gustafson E., Hammond S., Harley J.L.,  
 RA Hart E., Heath P.D., Ho T.P., Hopkins B., Horne J., Howden P.J.,  
 RA Hickle E., Hynds C., Johnson C., Johnson D., Kana A., Kay M.,  
 RA Kimberley A.M., Kershaw J.K., Kokkinnik M., Laird G., Lawlor S.,  
 RA Lee H.M., Leongamornlert D.A., Laird G., Lloyd C., Lloyd D.M.,  
 RA Loveland J., Lovell J., McLaren S., McEay K.E., McMurtry A.,  
 RA Mashrafi-Mohammadi M., Mathews L., Milne S., Nickerson T.,  
 RA Nguyen M., Overton-Larty E., Palmer S.A., Pearce A.V., Peck A.I.,  
 RA Pelan S., Phillimore B., Porter K., Rice C.M., Rogosin A., Rose M.T.,  
 RA Sarraffou T., Shira H.K., Showkeen R., Skuce C.D., Smith M.,  
 RA Standing L., Sycamore N., Tester J., Thorpe A., Torcasso W.,  
 RA Tracey A., Tromans A., Tsoias J., Wall M., Walsh J., Wang H.,  
 RA Wainstock K., West A.P., Willey D.L., Whitehead S.L., Wilming L.,  
 RA Wray P.W., Young L., Chen Y., Lovering R.C., Moschonas N.K.,  
 RA Webster R., Fectel K., Bentley D., Durbin R., Hubbard T.,  
 RA Doucette-Stamm L., Beck S., Smith D.R., Rogers J.;  
 RL "The DNA sequence and comparative analysis of human chromosome 10.";  
 RL Nature 429:375-381(2004).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Felingold B.A., Grouse L.H., Derge U.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shermen C.W., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scaplaton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loguelli N.A., Peters G.J., Adamson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallie D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).  
 RN [6]  
 RP IDENTIFICATION OF SDF-1ALPHA(3-67) AND SDF-1BETA(3-72) BY MASS

RP SPECTROMETRY, AND N-TERMINAL AND C-TERMINAL PROCESSING.  
 RX PubMed=14525775; DOI=10.1182/blood-2003-08-2857;  
 RA De la Luz Sierra M., Yang F., Narazaki M., Salvucci O., Davis D.,  
 RA Yarchan R., Zhang H.H., Fales H., Toato G.;  
 RT "Differential processing of stromal-derived factor-1alpha and beta  
 RT explains functional diversity.";  
 RL Blood 103:2452-2459(2004).  
 RN [7]  
 RP STRUCTURE BY NMR OF 22-88.  
 RX MEDLINE=96046030; PubMed=9384579;  
 RA Crump M.P., Gong U.H., Loetscher P., Rajaratnam K., Amara A.,  
 RA Azenzana-Seladedos F., Virelizier J.L., Baggiolini M., Sykes B.D.,  
 RA Clark-Lewis I.;  
 RT "Solution structure and basis for functional activity of stromal cell-  
 RT derived factor-1; dissociation of CXCR4 activation from binding and  
 RT inhibition of HIV-1.";  
 RL EMBO J. 16:6996-7007(1997).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.  
 RX MEDLINE=98284037; PubMed=9618518;  
 RA Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Stani M.A.,  
 RA Lolit E.;  
 RT "Crystal structure of chemically synthesized (N33A) stromal cell-  
 RT derived factor 1alpha, a potent ligand for the HIV-1 'fusin'  
 RT coreceptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).  
 CC -1- FUNCTION: Chemotactant active on T-lymphocytes, monocytes, but  
 CC not neutrophils. SDF-1-beta(3-72) and SDF-1-alpha(3-67) show a  
 CC reduced chemotactic activity. Binding to cell surface  
 CC proteoglycans seems to inhibit formation of SDF-1-alpha(3-67) and  
 CC thus to preserve activity on local sites.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Beta; Synonyms=SDF-1-beta(1-72);  
 CC IsoId=P48061-1; Sequence=Displayed;  
 CC Name=Alpha; Synonyms=SDF-1-alpha(1-68);  
 CC IsoId=P48061-2; Sequence=VSP 001056;  
 CC -1- PM: Processed forms SDF-1beta(3-72) and SDF-1alpha(3-67) are  
 CC produced after secretion by proteolytic cleavage of isoforms Beta  
 CC and Alpha, respectively. The N-terminal processing is probably  
 CC achieved by DPPI4. Isoform Alpha is first cleaved at the C-terminus  
 CC to yield a SDF-1-alpha(1-67) intermediate before being processed  
 CC at the N-terminus. The C-terminal processing of isoform Alpha is  
 CC reduced by binding to heparin and, probably, cell surface  
 CC proteoglycans.  
 CC -1- SIMILARITY: Belongs to the interleukin alpha (chemokine CXC)  
 CC family.  
 CC -----  
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 DR EMBL: U16752; AAA97434.1; -;  
 DR EMBL: L36033; AAB39332.1; -;  
 DR EMBL: L36034; AAB39333.1; -;  
 DR EMBL: U19495; AAB40516.1; -;  
 DR EMBL: AL137026; CAC10203.1; -;  
 DR EMBL: BC039893; AAB39893.1; -;  
 DR FTR: G01540; G01540.  
 DR PDB: 1A15; X-ray; A/B=22-88.  
 DR PDB: 1Q67; X-ray; A/B=22-88.  
 DR PDB: 1SDF; NMR; @=22-88.  
 DR PDB: 2SDF; NMR; @=22-88.  
 DR GENE: HNCN.10672; CXCL12.  
 DR NLM: 600835; -;  
 DR GO: GO:0008009; F:chemokine activity; TAS.  
 DR GO: GO:0005102; F:receptor binding; TAS.  
 DR GO: GO:0006874; P:calcium ion homeostasis; TAS.

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DR GO:0007155; P:cell adhesion; TAS.
DR GO:0006935; P:chemotaxis; TAS.
DR GO:0008015; P:circulation; TAS.
DR GO:0007165; P:G-protein coupled receptor protein signalin. . .; TAS.
DR GO:0008055; P:immune response; TAS.
DR GO:0008065; P:regulation of actin polymerization and/or d. . .; TAS.
DR GO:0009615; P:response to virus; TAS.
DR GO:0007165; P:signal transduction; TAS.
DR InterPro: IPR02473; C-X-C/Interlkn_8.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00436; INTERLEUKIN8.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
DR 3D-structure; Alternative splicing; Chemotaxis; Cytokine;
DR Growth factor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 93 Stromal cell-derived factor 1.
FT CHAIN 24 93 SDF-1beta(3-72).
FT CHAIN 24 88 SDF-1alpha(3-67).
FT DISULFID 30 55
FT DISULFID 32 71
FT VASAPIC 90 93 Missing (in isoform Alpha).
FT STRAND 36 36 /FtId=VSP_001056.
FT HELIX 41 43
FT STRAND 44 50
FT TURN 53 54
FT TURN 59 63
FT TURN 64 66
FT STRAND 69 72
FT TURN 74 75
FT HELIX 77 82
FT TURN 83 83
FT HELIX 84 87
SQ SEQUENCE 93 AA; 10666 MW; 505B5A29C2B44E8D CRC64;

Query Match 66.9%; Score 117; DB 1; Length 93;
Best Local Similarity 40.3%; Pred. No. 6.3e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSRCPRCFFGG-----GGKMKIQE 24
DB 22 KPVSLSRCPRCFFGVHVARANKILNTPNCALQIVARLKNRNQVCIDPKLKIQE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 11
Q6EKW4 PRELIMINARY; PRT; 116 AA.
AC Q6EKW4;
DT 01-OCT-2004 (TREMblrel. 28, Created)
DT 01-OCT-2004 (TREMblrel. 28, Last sequence update)
DT 01-OCT-2004 (TREMblrel. 28, Last annotation update)
DE CXC12 chemokine.
GN Name=CXC12;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CX NCBI_TaxId=9623;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed15242943;
RA Ledger T.N., Pinton P., Bourges D., Rouni P., Salmon H., Oswald I.P.;
RT "Development of a macroarray to specifically analyze immunological
RT gene expression in swine."
RL Clin. Diagn. Lab. Immunol. 11:691-698 (2004).
SQ EMBL; AY312066; AA084094.1; -.
SEQUENCE 116 AA; 12622 MW; 2A1BC0551C2BEAB CRC64;

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Query Match 66.9%; Score 117; DB 2; Length 116;
Best Local Similarity 40.3%; Pred. No. 7.8e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSRCPRCFFGG-----GGKMKIQE 24
DB 22 KPVSLSRCPRCFFGVHVARANKILNTPNCALQIVARLKNRNQVCIDPKLKIQE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 12
Q80ZM4 PRELIMINARY; PRT; 137 AA.
AC Q80ZM4;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Cxc12 protein.
GN Name=Cxc12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Alecnul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toobyuki S., Carninci P., Prange C.,
RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McEwan P.V., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Vallier J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallie D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046827; AA046827.1; -.
DR HSSP; P48061; ISDF.
DR MGD; MGI:103556; Cxc12.
DR GO:0008009; P:chemokine activity; IDA.
DR GO:0007420; P:brain development; IDA.
DR GO:0007281; P:germ cell development; IDA.
DR GO:0008354; P:germ cell migration; IDA.
DR GO:0050930; P:induction of positive chemotaxis; IDA.
DR GO:0030335; P:positive regulation of cell migration; IDA.
DR GO:0042098; P:T-cell proliferation; IMP.
DR InterPro: IPR02473; C-X-C/Interlkn_8.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 137 AA; 15529 MW; 04B47DAB6904DF77 CRC64;

Query Match 66.9%; Score 117; DB 2; Length 137;

```



GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: January 4, 2005, 15:43:59 ; Search time 61.9672 Seconds  
(without alignments)  
173.671 Million cell updates/sec

Title: US-10-086-177a-12

Perfect score: 169  
Sequence: 1 KPVSLSYRCRCRFGGGLKWIQVLEKALN 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: A\_Geneseq\_23Sep04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	100.0	30	5	AAB47694
2	169	100.0	30	5	AAB47692
3	158.5	93.8	31	3	AAB28545
4	158.5	93.8	31	5	AAB47693
5	158.5	93.8	31	5	AAB47686
6	158.5	93.8	31	5	AAB47706
7	158.5	93.8	31	5	AAB47702
8	158.5	93.8	31	5	AAB47717
9	158.5	93.8	31	5	AAB47715
10	158.5	93.8	31	5	AAB47707
11	158.5	93.8	31	5	AAB47716
12	158.5	93.8	31	5	AAB47695
13	158.5	93.8	31	5	AAB47700
14	158.5	93.8	31	5	AAB47703
15	158.5	93.8	31	5	AAB47714
16	158.5	93.8	31	5	AAB47701
17	157.5	93.2	33	5	AAB47698
18	157.5	93.2	33	5	AAB47696
19	157	92.9	34	5	AAB47697
20	157	92.9	34	5	AAB47699
21	155.5	92.0	31	5	AAB47705
22	155.5	92.0	31	5	AAB47704
23	149.5	88.0	31	5	AAM48698
24	148	87.6	34	5	AAM48699
25	138.5	82.0	27	3	AAB28544

26	132.5	78.4	25	3	AAB28546	AAB28546 Chemokine
27	130	76.9	28	5	AAM48673	AAM48673 CXCR4 pep
28	128.5	76.0	31	5	AAM48674	AAM48674 CXCR4 pep
29	125	74.0	28	5	AAM48676	AAM48676 CXCR4 pep
30	123.5	73.1	31	5	AAM48680	AAM48680 CXCR4 pep
31	123	72.8	28	5	AAM48678	AAM48678 CXCR4 pep
32	123	72.8	28	5	AAM48675	AAM48675 CXCR4 pep
33	121.5	71.9	31	5	AAM48682	AAM48682 CXCR4 pep
34	121.5	71.9	31	5	AAM48682	AAM48682 CXCR4 pep
35	120	71.0	28	5	AAM48677	AAM48677 CXCR4 pep
36	118.5	70.1	31	5	AAM48681	AAM48681 CXCR4 pep
37	118.5	70.1	67	2	AAM50760	AAM50760 Peptide w
38	118.5	70.1	67	2	AAY06726	AAY06726 Amino aci
39	118.5	70.1	67	2	AAY06743	AAY06743 SDF-1 alp
40	118.5	70.1	67	2	AAY06741	AAY06741 SDF-1 alp
41	118.5	70.1	67	2	AAY34092	AAY34092 Native sc
42	118.5	70.1	67	3	AAY67594	AAY67594 SDF-1 alp
43	118.5	70.1	67	5	AAB47680	AAB47680 SDF-1 alp
44	118.5	70.1	67	5	AAB47689	AAB47689 SDF-1 alp
45	118.5	70.1	67	7	ADP79402	ADP79402 Chemokine

## ALIGNMENTS

RESULT 1	
AAB47694	AAB47694 standard; peptide; 30 AA.
ID	AAB47694; (first entry)
AC	30-JAN-2002
DT	SDF-1(1-14) - (G)3 - SDF-1(55-67) amide.
DE	Hematopoietic cell; multiplications; CXCR4 chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.
KM	Synthetic.
OS	
XX	
FT	Key Modified-site Location/Qualifiers
FT	Modified-site 30 /note="C-terminal amide"
FT	
XX	
PN	WO200176615-A2.
XX	
PD	18-OCT-2001.
XX	
PF	12-APR-2001; 2001WO-CA000540.
XX	
PR	12-APR-2000; 2000CA-02305036.
PR	14-SEP-2000; 2000US-0232425P.
PR	23-FEB-2001; 2001CA-02335109.
XX	
PA	(UYBR-) UNIV BRITISH COLUMBIA.
PA	(CHEM-) CHEMOKINE THERAPEUTICS CORP.
PI	Safari H, Mezrouk A, Arab L, Tudan CR, Saxena G, Eaves CJ, Cashman J, Clark-Lewis I,
PI	WPI, 2002-025882/03.
XX	
DR	
XX	
PT	CXCR4 receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents, are useful for bone marrow or peripheral blood stem cell transplantation.
PT	
XX	
PS	Example 1; Page 42; 74pp; English.
XX	
CC	The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXCR4 chemokine receptor 4

CC (CXCR4) agonists to the cells. These peptides are based on stromal cell  
CC derived factor one (SDF-1) with some also containing sequences derived  
CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be  
CC used to reduce susceptibility of hematopoietic cells to a cytotoxic  
CC agent, by administering one of the agonist peptides to the cells prior to  
CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist  
CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic  
CC agent, particularly in a patient with cancer requiring autologous or  
CC allogenic bone marrow or peripheral blood stem cell transplantation, or  
CC an autoimmune disease

XX SQ Sequence 30 AA;

Query Match Best Local Similarity 100.0%; Score 169; DB 5; Length 30;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPGCGGLKWIQETLEKALN 30  
Db 1 KPVSLSYRCPGCGGLKWIQETLEKALN 30

RESULT 2

AAAB7692 standard; peptide; 30 AA.

XX AAB47692;

XX 30-JAN-2002 (first entry)

XX SDF-1(1-14) - (G)3 - SDF-1(55-67) acid.

XX Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;  
KM agonist; stromal cell derived factor one; SDF-1; autoimmune disease;  
KM macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;  
KM allogenic; bone marrow; stem cell; transplantation.

XX Synthetic.

XX WO200176615-A2.

XX 18-OCT-2001.

XX 12-APR-2001; 2001WO-CA000540.

XX 12-APR-2000; 2000CA-02305036.

XX 14-SEP-2000; 2000US-0232425P.

XX 23-FEB-2001; 2001CA-02335109.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Reeves CJ;

XX Cashman J, Clark-Lewis I;

XX WPI; 2002-025882/03.

XX CXC receptor 4 agonists that reduces hematopoietic cell multiplication

XX and susceptibility to cytotoxic agents, are useful for bone marrow or

XX peripheral blood stem cell transplantation.

XX Example 1; Page 42; 74pp; English.

XX The sequences given in AAB47680-717 represent peptides which may be used

XX in the method of the invention for reducing the rate of hematopoietic

XX cell multiplication. These peptides act as CXC chemokine receptor 4

XX (CXCR4) agonists to the cells. These peptides are based on stromal cell

XX derived factor one (SDF-1) with some also containing sequences derived

XX from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be

XX used to reduce susceptibility of hematopoietic cells to a cytotoxic

XX agent, by administering one of the agonist peptides to the cells prior to

XX or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist

XX is used to reduce susceptibility of hematopoietic cells to a cytotoxic

CC agent, particularly in a patient with cancer requiring autologous or

CC allogenic bone marrow or peripheral blood stem cell transplantation, or

CC an autoimmune disease

XX SQ Sequence 30 AA;

QY 1 KPVSLSYRCPGCGGLKWIQETLEKALN 30

Db 1 KPVSLSYRCPGCGGLKWIQETLEKALN 30

RESULT 3

AAAB28545 standard; peptide; 31 AA.

XX AAB28545;

XX 08-FEB-2001 (first entry)

XX Chemokine-derived synthetic peptide #5.

XX Chemokine-derived synthetic peptide; anti-HIV;

XX stromal cell-derived factor-1; SDF-1; Human immunodeficiency virus-1;

XX HIV-1; CXC chemokine receptor 4; CXCR4.

XX Synthetic.

XX WO200059928-A1.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US009236.

XX 07-APR-1999; 99US-0128106P.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Huang Z, Luo Z, Zhou N, Luo J;

XX WPI; 2000-686931/67.

XX Novel synthetic chemokine peptides of stromal cell derived factor useful

XX for inhibiting HIV-1 entry and infection via CXC chemokine receptor-4,

XX and in HIV infection treatment and prophylaxis.

XX Claim 14; Page 43; 56pp; English.

XX The present sequence is a synthetic chemokine peptide of the chemokine

XX stromal cell-derived factor-1 (SDF-1). It is useful for inhibiting the

XX entry of Human immunodeficiency virus-1 (HIV-1) into CXC chemokine

XX receptor 4 (CXCR4)-expressing cells and for treating HIV infection. The

XX novel SDF-1 derived synthetic peptides have enhanced activity over

XX separate peptides derived only from the N-terminal segment of SDF-1 or

XX derived only from the C-terminal region of SDF-1

XX SQ Sequence 31 AA;

QY 1 KPVSLSYRCPGCGGLKWIQETLEKALN 30

Db 1 KPVSLSYRCPGCGGLKWIQETLEKALN 31

RESULT 4

AAAB7693 standard; peptide; 31 AA.

XX AAB47693;  
 AC 30-JAN-2002 (first entry)  
 DT SDF-1(1-14) - (G)4 - SDF-1(55-67) acid.  
 DE  
 XX  
 XX Hematopoietic cell; multiplication; CXK chemokine receptor 4; CXCR4;  
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;  
 KM macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;  
 KW allogenic; bone marrow; stem cell; transplantation.  
 XX  
 XX Synthetic.  
 OS  
 XX W0200176615-A2.  
 PN 18-OCT-2001.  
 PD  
 XX 12-APR-2001; 2001WO-CA000540.  
 PF  
 XX 12-APR-2000; 2000CA-02305036.  
 PR 14-SEP-2000; 2000US-0232425P.  
 PR 23-FEB-2001; 2001CA-02335109.  
 XX  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;  
 PI Cashman J, Clark-Lewis I;  
 PI  
 XX WPI; 2002-025882/03.  
 DR  
 XX CXK receptor 4 agonists that reduces hematopoietic cell multiplication  
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or  
 PT peripheral blood stem cell transplantation.  
 PS  
 XX Example 1; Page 42; 74pp; English.  
 XX  
 CC The sequences given in AAB47680-717 represent peptides which may be used  
 CC in the method of the invention for reducing the rate of hematopoietic  
 CC cell multiplication. These peptides act as CXK chemokine receptor 4  
 CC (CXCR4) agonists to the cells. These peptides are based on stromal cell  
 CC derived factor one (SDF-1) with some also containing sequences derived  
 CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be  
 CC used to reduce susceptibility of hematopoietic cells to a cytotoxic  
 CC agent, by administering one of the agonist peptides to the cells prior to  
 CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist  
 CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic  
 CC agent, particularly in a patient with cancer requiring autologous or  
 CC allogenic bone marrow or peripheral blood stem cell transplantation, or  
 CC an autoimmune disease  
 CC  
 XX  
 SQ Sequence 31 AA;  
 Query Match 93.8%; Score 158.5; DB 5; Length 31;  
 Best Local Similarity 96.8%; Pred. No. 4.8e-15;  
 Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 KPVSLSYRCPCRFPGGGLKWIQYLEKALN 30  
 DB 1 KPVSLSYRCPCRFPGGGLKWIQYLEKALN 31  
 RESULT 5  
 AAB47686  
 ID AAB47686 standard; peptide; 31 AA.  
 XX  
 AC AAB47686;  
 XX  
 DT 30-JAN-2002 (first entry)  
 XX  
 DE SDF-1(1-14) - (G)4 - SDF-1(56-67).  
 XX

KW Hematopoietic cell; multiplication; CXK chemokine receptor 4; CXCR4;  
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;  
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;  
 KW allogenic; bone marrow; stem cell; transplantation.  
 XX  
 XX Synthetic.  
 OS  
 XX W0200176615-A2.  
 PN 18-OCT-2001.  
 PD  
 XX 12-APR-2001; 2001WO-CA000540.  
 PF  
 XX 12-APR-2000; 2000CA-02305036.  
 PR 14-SEP-2000; 2000US-0232425P.  
 PR 23-FEB-2001; 2001CA-02335109.  
 XX  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;  
 PI Cashman J, Clark-Lewis I;  
 PI  
 XX WPI; 2002-025882/03.  
 DR  
 XX CXK receptor 4 agonists that reduces hematopoietic cell multiplication  
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or  
 PT peripheral blood stem cell transplantation.  
 PS  
 XX Claim 8; Page 58; 74pp; English.  
 XX  
 CC The sequences given in AAB47680-717 represent peptides which may be used  
 CC in the method of the invention for reducing the rate of hematopoietic  
 CC cell multiplication. These peptides act as CXK chemokine receptor 4  
 CC (CXCR4) agonists to the cells. These peptides are based on stromal cell  
 CC derived factor one (SDF-1) with some also containing sequences derived  
 CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be  
 CC used to reduce susceptibility of hematopoietic cells to a cytotoxic  
 CC agent, by administering one of the agonist peptides to the cells prior to  
 CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist  
 CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic  
 CC agent, particularly in a patient with cancer requiring autologous or  
 CC allogenic bone marrow or peripheral blood stem cell transplantation, or  
 CC an autoimmune disease  
 CC  
 XX  
 SQ Sequence 31 AA;  
 Query Match 93.8%; Score 158.5; DB 5; Length 31;  
 Best Local Similarity 96.8%; Pred. No. 4.8e-15;  
 Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 KPVSLSYRCPCRFPGGGLKWIQYLEKALN 30  
 DB 1 KPVSLSYRCPCRFPGGGLKWIQYLEKALN 31  
 RESULT 6  
 AAB47706  
 ID AAB47706 standard; peptide; 31 AA.  
 XX  
 AC AAB47706;  
 XX  
 DT 30-JAN-2002 (first entry)  
 XX  
 DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-C9/C11-cyclic acid.  
 XX  
 KW Hematopoietic cell; multiplication; CXK chemokine receptor 4; CXCR4;  
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;  
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;  
 KW allogenic; bone marrow; stem cell; transplantation.  
 XX  
 OS Synthetic.  
 XX

FH Key Location/Qualifiers  
 FT Disulfide-bond 9.11  
 XX  
 PN WO200176615-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 12-APR-2001; 2001WO-CA000540.  
 XX  
 PR 12-APR-2000; 2000CA-02305036.  
 PR 14-SEP-2000; 2000US-0232425P.  
 PR 23-FEB-2001; 2001CA-02335109.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX  
 PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;  
 PI Cashman J, Clark-Lewis I;  
 DR WPI; 2002-025882/03.  
 XX  
 PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication  
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or  
 PT peripheral blood stem cell transplantation.  
 XX  
 PS Example 1; Page 44; 74pp; English.  
 XX  
 CC The sequences given in AAB47680-717 represent peptides which may be used  
 CC in the method of the invention for reducing the rate of hematopoietic  
 CC cell multiplication. These peptides act as CXC chemokine receptor 4  
 CC (CXCR4) agonists to the cells. These peptides are based on stromal cell  
 CC derived factor one (SDF-1) with some also containing sequences derived  
 CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be  
 CC used to reduce susceptibility of hematopoietic cells to a cytotoxic  
 CC agent, by administering one of the agonist peptides to the cells prior to  
 CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist  
 CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic  
 CC agent, particularly in a patient with cancer requiring autologous or  
 CC allogenic bone marrow or peripheral blood stem cell transplantation, or  
 CC an autoimmune disease  
 XX  
 SQ Sequence 31 AA;  
 Query Match 93.8%; Score 158.5; DB 5; Length 31;  
 Best Local Similarity 96.8%; Pred. No. 4.8e-15;  
 Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 KPVSLSYRCRCRFP-GGGLKWIQIYLEKALN 30  
 Db 1 KPVSLSYRCRCRFPGGGGLKWIQIYLEKALN 31  
 RESULT 7  
 AAB47702  
 ID AAB47702 standard; peptide; 31 AA.  
 XX  
 AC AAB47702;  
 XX  
 DT 30-JAN-2002 (first entry)  
 XX  
 DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-E24/K28-cyclic amide.  
 XX  
 KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;  
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;  
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;  
 KW allogenic; bone marrow; stem cell; transplantation.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 24.28  
 FT /note="Joined by side chain cyclization using lactam  
 FT formation"

FT Modified-site 31  
 FT /note="C-terminal amide"  
 XX  
 PN WO200176615-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 12-APR-2001; 2001WO-CA000540.  
 XX  
 PR 12-APR-2000; 2000CA-02305036.  
 PR 14-SEP-2000; 2000US-0232425P.  
 PR 23-FEB-2001; 2001CA-02335109.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX  
 PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;  
 PI Cashman J, Clark-Lewis I;  
 DR WPI; 2002-025882/03.  
 XX  
 PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication  
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or  
 PT peripheral blood stem cell transplantation.  
 XX  
 PS Example 1; Page 43; 74pp; English.  
 XX  
 CC The sequences given in AAB47680-717 represent peptides which may be used  
 CC in the method of the invention for reducing the rate of hematopoietic  
 CC cell multiplication. These peptides act as CXC chemokine receptor 4  
 CC (CXCR4) agonists to the cells. These peptides are based on stromal cell  
 CC derived factor one (SDF-1) with some also containing sequences derived  
 CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be  
 CC used to reduce susceptibility of hematopoietic cells to a cytotoxic  
 CC agent, by administering one of the agonist peptides to the cells prior to  
 CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist  
 CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic  
 CC agent, particularly in a patient with cancer requiring autologous or  
 CC allogenic bone marrow or peripheral blood stem cell transplantation, or  
 CC an autoimmune disease  
 XX  
 SQ Sequence 31 AA;  
 Query Match 93.8%; Score 158.5; DB 5; Length 31;  
 Best Local Similarity 96.8%; Pred. No. 4.8e-15;  
 Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 KPVSLSYRCRCRFP-GGGLKWIQIYLEKALN 30  
 Db 1 KPVSLSYRCRCRFPGGGGLKWIQIYLEKALN 31  
 RESULT 8  
 AAB47717  
 ID AAB47717 standard; peptide; 31 AA.  
 XX  
 AC AAB47717;  
 XX  
 DT 30-JAN-2002 (first entry)  
 XX  
 DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/E24-cyclic amide.  
 XX  
 KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;  
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;  
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;  
 KW allogenic; bone marrow; stem cell; transplantation.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 20.24  
 FT /note="Joined by side chain cyclization using lactam  
 FT formation"



FT Modified-site 31  
 /note= "C-terminal amide"  
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 XX  
 PN WO200176615-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 12-APR-2001; 2001WO-CA000540.  
 XX  
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 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX  
 PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;  
 PI Cashman J, Clark-Lewis I;  
 XX  
 DR WPI; 2002-025882/03.  
 XX  
 CC CXCR4 receptor 4 agonists that reduces hematopoietic cell multiplication  
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or  
 PT peripheral blood stem cell transplantation.  
 XX  
 PS Example 1; Page 47; 74pp; English.  
 XX  
 CC The sequences given in AAB47680-717 represent peptides which may be used  
 CC in the method of the invention for reducing the rate of hematopoietic  
 CC cell multiplication. These peptides act as CXCR4 chemokine receptor 4  
 CC (CXCR4) agonists to the cells. These peptides are based on stromal cell  
 CC derived factor one (SDF-1) with some also containing sequences derived  
 CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be  
 CC used to reduce susceptibility of hematopoietic cells to a cytotoxic  
 CC agent, by administering one of the agonist peptides to the cells prior to  
 CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist  
 CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic  
 CC agent, particularly in a patient with cancer requiring autologous or  
 CC allogenic bone marrow or peripheral blood stem cell transplantation, or  
 CC an autoimmune disease  
 CC  
 XX  
 SQ Sequence 31 AA;  
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 Query Match 93.8%; Score 158.5; DB 5; Length 31;  
 Best Local Similarity 96.8%; Pred. No. 4.8e-15;  
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 QY 1 KPVSLSYRCPCRFPGGGGLKWIQIYLEKALN 30  
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 XX  
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 ID AAB47715 standard; peptide; 31 AA.  
 XX  
 AC AAB47715;  
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 DT 30-JAN-2002 (first entry)  
 XX  
 DE SDF-1(1-14) - (G) 4 - SDF-1(55-67) amide.  
 XX  
 KW Hematopoietic cell; multiplication; CXCR4 chemokine receptor 4; CXCR4;  
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;  
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;  
 KW allogenic; bone marrow; stem cell; transplantation.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 31  
 FT /note= "C-terminal amide"  
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PN WO200176615-A2.  
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 PF 12-APR-2001; 2001WO-CA000540.  
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 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX  
 PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;  
 PI Cashman J, Clark-Lewis I;  
 XX  
 DR WPI; 2002-025882/03.  
 XX  
 CC CXCR4 receptor 4 agonists that reduces hematopoietic cell multiplication  
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or  
 PT peripheral blood stem cell transplantation.  
 XX  
 PS Example 1; Page 47; 74pp; English.  
 XX  
 CC The sequences given in AAB47680-717 represent peptides which may be used  
 CC in the method of the invention for reducing the rate of hematopoietic  
 CC cell multiplication. These peptides act as CXCR4 chemokine receptor 4  
 CC (CXCR4) agonists to the cells. These peptides are based on stromal cell  
 CC derived factor one (SDF-1) with some also containing sequences derived  
 CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be  
 CC used to reduce susceptibility of hematopoietic cells to a cytotoxic  
 CC agent, by administering one of the agonist peptides to the cells prior to  
 CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist  
 CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic  
 CC agent, particularly in a patient with cancer requiring autologous or  
 CC allogenic bone marrow or peripheral blood stem cell transplantation, or  
 CC an autoimmune disease  
 CC  
 XX  
 SQ Sequence 31 AA;  
 XX  
 Query Match 93.8%; Score 158.5; DB 5; Length 31;  
 Best Local Similarity 96.8%; Pred. No. 4.8e-15;  
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 QY 1 KPVSLSYRCPCRFPGGGGLKWIQIYLEKALN 30  
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 DB 1 KPVSLSYRCPCRFPGGGGLKWIQIYLEKALN 31  
 XX  
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 ID AAB47707 standard; peptide; 31 AA.  
 XX  
 AC AAB47707;  
 XX  
 DT 30-JAN-2002 (first entry)  
 XX  
 DE SDF-1(1-14) - (G) 4 - SDF-1(55-67)-C9/C11-cyclic amide.  
 XX  
 KW Hematopoietic cell; multiplication; CXCR4 chemokine receptor 4; CXCR4;  
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;  
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;  
 KW allogenic; bone marrow; stem cell; transplantation.  
 XX  
 OS Synthetic.  
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 FH Key Location/Qualifiers  
 FT Disulfide-bond 9.11  
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PD 18-OCT-2001.  
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XX 12-APR-2001; 2001WO-CA000540.  
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PR 12-APR-2000; 2000CA-02305036.  
PR 14-SEP-2000; 2000US-0232425P.  
PR 23-FEB-2001; 2001CA-02335109.  
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PA (UYBR-) UNIV BRITISH COLUMBIA.  
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
XX  
PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;  
PI Cashman J, Clark-Lewis I;  
XX  
XX WPI; 2002-025882/03.  
XX  
PT CXCR4 receptor 4 agonists that reduces hematopoietic cell multiplication  
PT and susceptibility to cytotoxic agents, are useful for bone marrow or  
PT peripheral blood stem cell transplantation.  
XX  
XX  
PS Example 1; Page 44; 74pp; English.  
XX  
CC The sequences given in AAB47680-717 represent peptides which may be used  
CC in the method of the invention for reducing the rate of hematopoietic  
CC cell multiplication. These peptides act as CXCR4 chemokine receptor 4  
CC (CXCR4) agonists to the cells. These peptides are based on stromal cell  
CC derived factor one (SDF-1) with some also containing sequences derived  
CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be  
CC used to reduce susceptibility of hematopoietic cells to a cytotoxic  
CC agent, by administering one of the agonist peptides to the cells prior to  
CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist  
CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic  
CC agent, particularly in a patient with cancer requiring autologous or  
CC allogenic bone marrow or peripheral blood stem cell transplantation, or  
CC an autoimmune disease  
XX  
SQ Sequence 31 AA;  
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Query Match 93.8%; Score 158.5; DB 5; Length 31;  
Best Local Similarity 96.8%; Pred. No. 4.8e-15;  
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XX  
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ID AAB47716 standard; peptide; 31 AA.  
XX  
AC AAB47716;  
XX  
DT 30-JAN-2002 (first entry)  
XX  
DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-E24/K28-cyclic amide.  
XX  
KW Hematopoietic cell; multiplication; CXCR4 chemokine receptor 4; CXCR4;  
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;  
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;  
KW allogenic; bone marrow; stem cell; transplantation.  
XX  
OS Synthetic.  
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FH Key Location/Qualifiers  
FT Modified-site 24..28  
FT /note= "Joined by side chain cyclization using lactam  
FT formation"  
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FT /note= "C-terminal amide"  
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XX WO200176615-A2.  
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PD 18-OCT-2001.  
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XX 12-APR-2001; 2001WO-CA000540.  
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PR 14-SEP-2000; 2000US-0232425P.  
PR 23-FEB-2001; 2001CA-02335109.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
XX  
PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;  
PI Cashman J, Clark-Lewis I;  
XX  
XX WPI; 2002-025882/03.  
XX  
PT CXCR4 receptor 4 agonists that reduces hematopoietic cell multiplication  
PT and susceptibility to cytotoxic agents, are useful for bone marrow or  
PT peripheral blood stem cell transplantation.  
XX  
XX  
PS Example 1; Page 47; 74pp; English.  
XX  
CC The sequences given in AAB47680-717 represent peptides which may be used  
CC in the method of the invention for reducing the rate of hematopoietic  
CC cell multiplication. These peptides act as CXCR4 chemokine receptor 4  
CC (CXCR4) agonists to the cells. These peptides are based on stromal cell  
CC derived factor one (SDF-1) with some also containing sequences derived  
CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be  
CC used to reduce susceptibility of hematopoietic cells to a cytotoxic  
CC agent, by administering one of the agonist peptides to the cells prior to  
CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist  
CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic  
CC agent, particularly in a patient with cancer requiring autologous or  
CC allogenic bone marrow or peripheral blood stem cell transplantation, or  
CC an autoimmune disease  
XX  
SQ Sequence 31 AA;  
XX  
Query Match 93.8%; Score 158.5; DB 5; Length 31;  
Best Local Similarity 96.8%; Pred. No. 4.8e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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DB 1 KPVSLSYRCPGRFFGGGGLKWIQIYLEKALN 31  
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XX  
AC AAB47695;  
XX  
DT 30-JAN-2002 (first entry)  
XX  
DE SDF-1(1-14) - (G)4 - SDF-1(55-67) amide.  
XX  
KW Hematopoietic cell; multiplication; CXCR4 chemokine receptor 4; CXCR4;  
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;  
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;  
KW allogenic; bone marrow; stem cell; transplantation.  
XX  
OS Synthetic.  
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FH Key Location/Qualifiers  
FT Modified-site 31  
FT /note= "C-terminal amide"  
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XX WO200176615-A2.  
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 PR 23-FEB-2001; 2001CA-02335109.  
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 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ,  
 PI Cashman J, Clark-Lewis I;  
 DR WPI; 2002-025882/03.  
 XX  
 PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication  
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or  
 PT peripheral blood stem cell transplantation.  
 XX  
 PS Example 1; Page 42; 74pp; English.  
 XX  
 CC The sequences given in AAB47680-717 represent peptides which may be used  
 CC in the method of the invention for reducing the rate of hematopoietic  
 CC cell multiplication. These peptides act as CXC chemokine receptor 4  
 CC (CXCR4) agonists to the cells. These peptides are based on stromal cell  
 CC derived factor one (SDF-1) with some also containing sequences derived  
 CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be  
 CC used to reduce susceptibility of hematopoietic cells to a cytotoxic  
 CC agent, by administering one of the agonist peptides to the cells prior to  
 CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist  
 CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic  
 CC agent, particularly in a patient with cancer requiring autologous or  
 CC allogenic bone marrow or peripheral blood stem cell transplantation, or  
 CC an autoimmune disease  
 XX  
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 AC AAB47700;  
 XX  
 DT 30-JAN-2002 (first entry)  
 XX  
 DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-B24/K28-cyclic acid.  
 XX  
 KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;  
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;  
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;  
 KW allogenic; bone marrow; stem cell; transplantation.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 24..28  
 FT /note= "Joined by side chain cyclization using lactam  
 FT formation"  
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PR 14-SEP-2000; 2000US-0232425P.  
 PR 23-FEB-2001; 2001CA-02335109.  
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 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ,  
 PI Cashman J, Clark-Lewis I;  
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 XX  
 PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication  
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or  
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 XX  
 PS Example 1; Page 43; 74pp; English.  
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 CC The sequences given in AAB47680-717 represent peptides which may be used  
 CC in the method of the invention for reducing the rate of hematopoietic  
 CC cell multiplication. These peptides act as CXC chemokine receptor 4  
 CC (CXCR4) agonists to the cells. These peptides are based on stromal cell  
 CC derived factor one (SDF-1) with some also containing sequences derived  
 CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be  
 CC used to reduce susceptibility of hematopoietic cells to a cytotoxic  
 CC agent, by administering one of the agonist peptides to the cells prior to  
 CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist  
 CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic  
 CC agent, particularly in a patient with cancer requiring autologous or  
 CC allogenic bone marrow or peripheral blood stem cell transplantation, or  
 CC an autoimmune disease  
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 KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;  
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;  
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;  
 KW allogenic; bone marrow; stem cell; transplantation.  
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 FT formation"  
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 FT /note= "C-terminal amide"  
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PR 14-SEP-2000; 2000US-0232425P.
XX 23-FEB-2001; 2001CA-02335109.
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI Cashman J, Clark-Lewis I;
XX WPI; 2002-025882/03.
XX
XX CXC receptor 4 agonists that reduces hematopoietic cell multiplication
PT and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation.
XX
XX Example 1; Page 43; 74pp; English.
XX
XX The sequences given in AAB47680-717 represent peptides which may be used
CC in the method of the invention for reducing the rate of hematopoietic
CC cell multiplication. These peptides act as CXC chemokine receptor 4
CC (CXCR4) agonists to the cells. These peptides are based on stromal cell
CC derived factor one (SDF-1) with some also containing sequences derived
CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be
CC used to reduce susceptibility of hematopoietic cells to a cytotoxic
CC agent, by administering one of the agonist peptides to the cells prior to
CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist
CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic
CC agent, particularly in a patient with cancer requiring autologous or
CC allogenic bone marrow or peripheral blood stem cell transplantation, or
CC an autoimmune disease
XX
XX Sequence 31 AA;
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XX 30-JAN-2002 (first entry)
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XX Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;
KW allogenic; bone marrow; stem cell; transplantation.
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PR 23-FEB-2001; 2001CA-02335109.
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XX (UYBR-) UNIV BRITISH COLUMBIA.
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;

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PI Cashman J, Clark-Lewis I;
XX
XX WPI; 2002-025882/03.
DR
XX
XX CXC receptor 4 agonists that reduces hematopoietic cell multiplication
PT and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation.
XX
XX Example 1; Page 47; 74pp; English.
XX
XX The sequences given in AAB47680-717 represent peptides which may be used
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CC cell multiplication. These peptides act as CXC chemokine receptor 4
CC (CXCR4) agonists to the cells. These peptides are based on stromal cell
CC derived factor one (SDF-1) with some also containing sequences derived
CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be
CC used to reduce susceptibility of hematopoietic cells to a cytotoxic
CC agent, by administering one of the agonist peptides to the cells prior to
CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist
CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic
CC agent, particularly in a patient with cancer requiring autologous or
CC allogenic bone marrow or peripheral blood stem cell transplantation, or
CC an autoimmune disease
XX
XX Sequence 31 AA;
SQ
Query Match 93.8%; Score 158.5; DB 5; Length 31;
Best Local Similarity 96.8%; Pred. No. 4.8e-15;
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QY 1 KPVSLSYRCPCRF-GGGLKWIQIYLEKALN 30
DB 1 KPVSLSYRCPCRFGGGGLKWIQIYLEKALN 31
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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: January 4, 2005, 15:43:59 ; Search time 27.0492 Seconds

(without alignments)  
73.553 Million cell updates/sec

Title: US-10-086-177a-12

Perfect score: 169  
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Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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3	132.5	78.4	25	4	US-09-543-940-6
4	118.5	70.1	89	1	US-08-181-556-2
5	118.5	70.1	89	1	US-08-323-084A-1
6	118.5	70.1	89	1	US-08-323-084A-1
7	118.5	70.1	89	1	US-09-461-912A-46
8	118.5	70.1	93	1	US-08-323-084A-5
9	118.5	70.1	93	1	US-08-674-008-5
10	118.5	70.1	93	4	US-09-312-283C-421
11	118.5	70.1	93	4	US-09-919-497-95
12	118.5	70.1	166	4	US-09-646-028-5
13	118.5	70.1	177	4	US-09-646-028-54
14	118.5	70.1	326	3	US-08-808-720-3
15	118.5	70.1	326	3	US-09-467-638-3
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18	118.5	70.1	339	4	US-09-646-028-55
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21	69	40.8	13	4	US-09-543-940-9
22	62	36.7	10	4	US-09-543-940-8
23	59.5	35.2	1084	4	US-09-221-013A-8
24	57	33.7	97	4	US-09-270-767-39706
25	57	33.7	97	4	US-09-270-767-54923
26	57	33.7	192	4	US-09-270-767-32013
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28	55	32.5	10	4	US-09-543-940-12	Sequence 12, Appl
29	52	30.8	974	3	US-08-960-048-6	Sequence 6, Appl
30	52	30.8	974	4	US-09-838-586-6	Sequence 6, Appl
31	51.5	30.5	504	4	US-09-252-991A-32272	Sequence 3272, A
32	49.5	29.3	535	4	US-09-252-991A-25662	Sequence 25662, A
33	49.5	29.3	588	3	US-08-481-190-16	Sequence 16, Appl
34	49.5	29.3	588	5	PCT-US93-00869-16	Sequence 16, Appl
35	49.5	29.3	1129	4	US-09-023-905A-2	Sequence 2, Appl
36	49.5	29.3	1151	4	US-09-023-905A-4	Sequence 4, Appl
37	49	29.0	416	1	US-08-117-083-61	Sequence 61, Appl
38	48.5	28.7	685	3	US-08-960-048-7	Sequence 7, Appl
39	48.5	28.7	685	4	US-09-838-586-7	Sequence 7, Appl
40	48	28.4	436	4	US-09-252-991A-28555	Sequence 28555, A
41	48	28.4	542	4	US-09-489-039A-8620	Sequence 8620, Ap
42	47.5	28.1	305	4	US-09-252-991A-26204	Sequence 26204, A
43	47.5	28.1	927	4	US-09-252-991A-20340	Sequence 20340, A
44	47	27.8	22	4	US-09-762-724-25	Sequence 25, Appl
45	47	27.8	71	4	US-09-270-767-56665	Sequence 56665, A

## ALIGNMENTS

RESULT 1  
US-09-543-940-5  
Sequence 5, Application US/09543940  
Patent No. 6613742  
GENERAL INFORMATION:  
APPLICANT: Huang, Ziwei  
APPLICANT: Luo, Zhaoen  
APPLICANT: Zhou, Naiping  
APPLICANT: Luo, Jiansong  
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides  
FILE REFERENCE: 8321-40  
CURRENT APPLICATION NUMBER: US/09/543,940  
CURRENT FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: 60/128,106  
PRIOR FILING DATE: 1999-04-07  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 5  
LENGTH: 31  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide containing segments from N- and C-terminal  
US-09-543-940-5  
Query Match 93.8%; Score 158.5; DB 4; Length 31;  
Best Local Similarity 96.8%; Pred. No. 2.6e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 KPVSLSTRCPFRFGGGLKWIQBYLEKALN 30  
DB 1 KPVSLSTRCPFRFGGGLKWIQBYLEKALN 31  
RESULT 2  
US-09-543-940-4  
Sequence 4, Application US/09543940  
Patent No. 6613742  
GENERAL INFORMATION:  
APPLICANT: Huang, Ziwei  
APPLICANT: Luo, Zhaoen  
APPLICANT: Zhou, Naiping  
APPLICANT: Luo, Jiansong  
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides  
FILE REFERENCE: 8321-40  
CURRENT APPLICATION NUMBER: US/09/543,940  
CURRENT FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: 60/128,106

PRIOR FILING DATE: 1999-04-07  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 4  
LENGTH: 27  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide containing segments from N- and C-terminal  
US-09-543-940-4

Query Match 82.0%; Score 138.5; DB 4; Length 27;  
Best Local Similarity 96.3%; Pred. No. 1.4e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 5 LSYRCPFRFGGGLKWIQEVLEKALN 30  
DB 1 LSYRCPFRFGGGLKWIQEVLEKALN 27

RESULT 3  
US-09-543-940-6  
Sequence 6, Application US/09543940  
Patent No. 6613742  
GENERAL INFORMATION:  
APPLICANT: Huang, Ziwei  
APPLICANT: Luo, Zhaoen  
APPLICANT: Zhou, Naiming  
APPLICANT: Luo, Jiansong  
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides  
FILE REFERENCE: 8321-40  
CURRENT APPLICATION NUMBER: US/09/543,940  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: 60/128,106  
PRIOR FILING DATE: 1999-04-07  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 6  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide containing segments from N- and C-terminal  
OTHER INFORMATION: regions of human SDF-1 protein  
US-09-543-940-6

Query Match 78.4%; Score 132.5; DB 4; Length 25;  
Best Local Similarity 96.2%; Pred. No. 8.8e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 5 LSYRCPFRFGGGLKWIQEVLEKALN 30  
DB 1 LSYRCPFRFGGGLKWIQEVLEKALN 25

RESULT 4  
US-08-181-556-2  
Sequence 2, Application US/08181556  
Patent No. 5525486  
GENERAL INFORMATION:  
APPLICANT: HONTO, Tasuku  
APPLICANT: TASHIRO, Kei  
APPLICANT: TADA, Hideaki  
TITLE OF INVENTION: PROCESS FOR CONSTRUCTING CDNA LIBRARY,  
TITLE OF INVENTION: AND NOVEL POLYPEPTIDE AND DNA CODING FOR THE SAME  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STEVENS, DAVIS, MILLER & MOSHER  
STREET: 515 No. 5525486th Washington Street (P.O. Box 1427)  
CITY: Alexandria

STATE: Virginia  
COUNTRY: USA  
ZIP: 22313  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/181,556  
FILING DATE: 14-JAN-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-22098  
FILING DATE: 14-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: POULOS III, James A.  
REGISTRATION NUMBER: 31714  
REFERENCE/DOCKET NUMBER: TPI/29088  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 549-7200  
TELEFAX: (703) 528-5313  
TELEX: 89-2746  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 89 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-181-556-2

Query Match 70.1%; Score 118.5; DB 1; Length 89;  
Best Local Similarity 40.3%; Pred. No. 2.9e-09;  
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPFRFGG-----GLKWIQEV 23  
DB 22 KPVSLSYRCPFRFGGSHIARANYKILNTPNCALQIVARLKNNNRQVCIIDPKWKIQEV 81

QY 24 YLEKALN 30  
DB 82 YLEKALN 88

RESULT 5  
US-08-323-084A-1  
Sequence 1, Application US/08323084A  
Patent No. 5563048  
GENERAL INFORMATION:  
APPLICANT: HONTO, TASUKU  
APPLICANT: SHIROZU, MICHIO  
APPLICANT: TADA, HIDEAKI  
TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/323,084A  
FILING DATE: 14-OCT-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 280505/1993  
FILING DATE: 14-OCT-1993

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)293-7060  
 TELEFAX: (202)293-7860  
 TELEX: 6491103  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 89 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-323-084A-1

Query Match 70.1%; Score 118.5; DB 1; Length 89;  
 Best Local Similarity 40.3%; Pred. No. 2.9e-09;  
 Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKXIOE 23  
 |||||  
 DB 22 KPVSLSYRCPCRFESHVARANVGHKLINTPNCALQIVARLKNNNRQVCIDPRLKXIOE 81  
 |||||  
 QY 24 YLEKALN 30  
 |||||  
 DB 82 YLEKALN 88

## RESULT 6

US-08-674-008-1  
 Sequence 1, Application US/08674008  
 Patent No. 5756084  
 GENERAL INFORMATION:

APPLICANT: HONJO, Tasaku  
 APPLICANT: SHIROZU, Michio  
 APPLICANT: TADA, Hideaki  
 TITLE OF INVENTION: HUMAN STROMAL DERIVED  
 TITLE OF INVENTION: FACTOR 1 AND 1 (As Amended)  
 NUMBER OF SEQUENCES: 20  
 CORRESPONDENCE ADDRESSES:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
 STREET: 2100 Pennsylvania Avenue, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20037-3202

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/674,008  
 FILING DATE: 1-JUL-1996  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/323,084  
 FILING DATE: 14-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 280505/1993  
 FILING DATE: 14-OCT-1993

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)293-7060  
 TELEFAX: (202)293-7860  
 TELEX: 6491103

INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 89 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-674-008-1

Query Match 70.1%; Score 118.5; DB 1; Length 89;  
 Best Local Similarity 40.3%; Pred. No. 2.9e-09;  
 Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKXIOE 23  
 |||||

DB 22 KPVSLSYRCPCRFESHVARANVGHKLINTPNCALQIVARLKNNNRQVCIDPRLKXIOE 81  
 |||||

QY 24 YLEKALN 30  
 |||||  
 DB 82 YLEKALN 88

## RESULT 7

US-09-461-912A-46  
 Sequence 46, Application US/09461912A  
 Patent No. 6708855  
 GENERAL INFORMATION:

APPLICANT: Stanton, Lawrence A.  
 APPLICANT: White, R. Tyler  
 APPLICANT: Damm, Deborah L.  
 APPLICANT: Lewicki, John A.  
 TITLE OF INVENTION: Methods for detection and use of  
 TITLE OF INVENTION: differentially expressed genes in disease states  
 FILE REFERENCE: SCIOS.011A  
 CURRENT FILING DATE: 1999-12-15  
 PRIOR APPLICATION NUMBER: US 60/113,008  
 PRIOR FILING DATE: 1998-12-18  
 NUMBER OF SEQ ID NOS: 48  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 46  
 LENGTH: 89  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-461-912A-46

Query Match 70.1%; Score 118.5; DB 4; Length 89;  
 Best Local Similarity 40.3%; Pred. No. 2.9e-09;  
 Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKXIOE 23  
 |||||

DB 22 KPVSLSYRCPCRFESHVARANVGHKLINTPNCALQIVARLKNNNRQVCIDPRLKXIOE 81  
 |||||

QY 24 YLEKALN 30  
 |||||  
 DB 82 YLEKALN 88

## RESULT 8

US-08-323-084A-5  
 Sequence 5, Application US/08323084A  
 Patent No. 5563048  
 GENERAL INFORMATION:

APPLICANT: HONJO, TASUKU  
 APPLICANT: SHIROZU, MICHIO  
 APPLICANT: TADA, HIDEAKI  
 TITLE OF INVENTION: No. 5563048e1 Polypeptides and DNAs encoding them  
 NUMBER OF SEQUENCES: 20  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
 STREET: 2100 Pennsylvania Avenue, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20037-3202

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/323,084A  
 FILING DATE:  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 280505/1993  
FILING DATE: 14-OCT-1993  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-323-084A-5

Query Match 70.1%; Score 118.5; DB 1; Length 93;  
Best Local Similarity 40.3%; Pred. No. 3e-09;  
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKWKIOE 23  
Db 22 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNRRQVCIDPKLWKIOE 81  
QY 24 YLEKALN 30  
Db 82 YLEKALN 88

RESULT 9  
US-08-674-008-5  
Sequence 5, Application US/08674008  
Patent No. 5756084  
GENERAL INFORMATION:  
APPLICANT: HONJO, Tasaku  
APPLICANT: SHIROZU, Michio  
TITLE OF INVENTION: HUMAN STROMAL DERIVED  
TITLE OF INVENTION: TADA, Hideaki  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20037-3302  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/674,008  
FILING DATE: 1-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/323,084  
FILING DATE: 14-OCT-1994  
PRIOR APPLICATION DATA: JP 280505/1993  
APPLICATION NUMBER: JP 280505/1993  
FILING DATE: 14-OCT-1993  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-674-008-5

Query Match 70.1%; Score 118.5; DB 1; Length 93;  
Best Local Similarity 40.3%; Pred. No. 3e-09;  
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKWKIOE 23  
Db 22 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNRRQVCIDPKLWKIOE 81  
QY 24 YLEKALN 30  
Db 82 YLEKALN 88

RESULT 10  
US-09-312-283C-421  
Sequence 421, Application US/09312283C  
Patent No. 6573095  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Ormest, Rene  
APPLICANT: Munison, James G.  
APPLICANT: Kumble, Krishanand D.  
TITLE OF INVENTION: Compositions Isolated from Skin Cells  
TITLE OF INVENTION: and Methods for Their Use  
FILE REFERENCE: 11000.1011c2  
CURRENT APPLICATION NUMBER: US/09/312,283C  
CURRENT FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 425  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 421  
LENGTH: 93  
TYPE: PRT  
ORGANISM: Mouse  
US-09-312-283C-421

Query Match 70.1%; Score 118.5; DB 4; Length 93;  
Best Local Similarity 40.3%; Pred. No. 3e-09;  
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKWKIOE 23  
Db 22 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNRRQVCIDPKLWKIOE 81  
QY 24 YLEKALN 30  
Db 82 YLEKALN 88

RESULT 11  
US-09-919-497-95  
Sequence 95, Application US/09919497  
Patent No. 6773883  
GENERAL INFORMATION:  
APPLICANT: Mutter, George L.  
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER  
FILE REFERENCE: B0801/7225  
CURRENT APPLICATION NUMBER: US/09/919,497  
CURRENT FILING DATE: 2001-07-31  
PRIOR APPLICATION NUMBER: US 60/221,735  
PRIOR FILING DATE: 2000-07-31  
NUMBER OF SEQ ID NOS: 100  
SOFTWARE: Patentin Version 3.0  
SEQ ID NO 95  
LENGTH: 93  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-919-497-95

Query Match 70.1%; Score 118.5; DB 4; Length 93;  
Best Local Similarity 40.3%; Pred. No. 3e-09;  
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;



QY 1 KPVSLSYRCPCRFPGG-----GLKXIOE 23  
DB 22 KPVSLSYRCPCRFESHVARANVGHKLINTPNCALQIVARLKNNNRQVCIDPGLKXIOE 81  
QY 24 YLEKALN 30  
DB 82 YLEKALN 88

RESULT 12  
US-09-646-028-5  
Sequence 5, Application US/09646028  
Patent No. 6562347  
GENERAL INFORMATION:  
APPLICANT: Kwak, Larry  
APPLICANT: Birsayn, Arya  
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF  
FILE REFERENCE: 14014.0316/P  
CURRENT APPLICATION NUMBER: US/09/646,028  
CURRENT FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: 60/077,745  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 166  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
US-09-646-028-5

Query Match 70.1%; Score 118.5; DB 4; Length 166;  
Best Local Similarity 40.3%; Pred. No. 5.4e-09;  
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKXIOE 23  
DB 22 KPVSLSYRCPCRFESHVARANVGHKLINTPNCALQIVARLKNNNRQVCIDPGLKXIOE 81  
QY 24 YLEKALN 30  
DB 82 YLEKALN 88

RESULT 13  
US-09-646-028-54  
Sequence 54, Application US/09646028  
Patent No. 6562347  
GENERAL INFORMATION:  
APPLICANT: Kwak, Larry  
APPLICANT: Birsayn, Arya  
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF  
FILE REFERENCE: 14014.0316/P  
CURRENT APPLICATION NUMBER: US/09/646,028  
CURRENT FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: 60/077,745  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 54  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
US-09-646-028-54

Query Match 70.1%; Score 118.5; DB 4; Length 177;  
Best Local Similarity 40.3%; Pred. No. 5.7e-09;

Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;  
QY 1 KPVSLSYRCPCRFPGG-----GLKXIOE 23  
DB 4 KPVSLSYRCPCRFESHVARANVGHKLINTPNCALQIVARLKNNNRQVCIDPGLKXIOE 63  
QY 24 YLEKALN 30  
DB 64 YLEKALN 70

RESULT 14  
US-08-808-720-3  
Sequence 3, Application US/08808720  
Patent No. 6100387  
GENERAL INFORMATION:  
APPLICANT: Herrmann, Steve  
APPLICANT: Swenberg, Stephen  
TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING  
TITLE OF INVENTION: CHEMOKINE DOMAINS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genetics Institute, Inc.  
STREET: 87 Cambridgepark  
CITY: Cambridge  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/808,720  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Sprunger, Suzanne  
REGISTRATION NUMBER: P-41,323  
REFERENCE/DOCKET NUMBER: G15291  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8284  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 326 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-808-720-3

Query Match 70.1%; Score 118.5; DB 3; Length 326;  
Best Local Similarity 40.3%; Pred. No. 1.1e-08;  
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKXIOE 23  
DB 20 KPVSLSYRCPCRFESHVARANVGHKLINTPNCALQIVARLKNNNRQVCIDPGLKXIOE 79  
QY 24 YLEKALN 30  
DB 80 YLEKALN 86

RESULT 15  
US-09-467-638-3  
Sequence 3, Application US/09467638  
Patent No. 6730296  
GENERAL INFORMATION:  
APPLICANT: Herrmann, Steve  
APPLICANT: Swenberg, Stephen

```

/ TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
/ TITLE OF INVENTION: CHEMOKINE DOMAINS
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genetics Institute, Inc.
/ STREET: 87 Cambridgepark
/ CITY: Cambridge
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02140
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/467,638
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/808,720
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sprunger, Suzanne
/ REGISTRATION NUMBER: P-41,323
/ REFERENCE/DOCKET NUMBER: G15291
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 498-8284
/ TELEFAX: (617) 876-5851
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 326 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-09-467-638-3

```

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Query Match 70.1%; Score 118.5; DB 4; Length 326;
Best Local Similarity 40.3%; Pred. No. 1.1e-06;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

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QY 1 KPVSLSTRCPGRFPFG-----GLKWIQE 23
   |||||
Db 20 KPVSLSTRCPGRFPESHVARANVGHILKILNTPNCALQIVARLKNNNRQVCIDPKLKIQE 79
   |||||
QY 24 YLEKALN 30
   |||||
Db 80 YLEKALN 86

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Search completed: January 4, 2005, 15:47:49  
 Job time : 30.0492 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 4, 2005, 15:46:58 ; Search time 97.8689 Seconds  
(without alignments)  
110.268 Million cell updates/sec

Title: US-10-086-177A-12

Perfect score: 169  
Sequence: 1 KPVSLSYRCPCRFGGGLKWIQRYLEKALN 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/prodata/1/pubppa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata/1/pubppa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/prodata/1/pubppa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/prodata/1/pubppa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/prodata/1/pubppa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/prodata/1/pubppa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/prodata/1/pubppa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/prodata/1/pubppa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/prodata/1/pubppa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/prodata/1/pubppa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/prodata/1/pubppa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/prodata/1/pubppa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/prodata/1/pubppa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/prodata/1/pubppa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/prodata/1/pubppa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/prodata/1/pubppa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/prodata/1/pubppa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/prodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	169	100.0	30 9 US-09-835-107-12	Sequence 12, Appl
2	169	100.0	30 9 US-09-835-107-14	Sequence 14, Appl
3	169	100.0	30 14 US-10-086-177A-12	Sequence 12, Appl
4	169	100.0	30 14 US-10-086-177A-14	Sequence 14, Appl
5	158.5	93.8	31 9 US-09-835-107-13	Sequence 13, Appl
6	158.5	93.8	31 9 US-09-835-107-15	Sequence 15, Appl
7	158.5	93.8	31 9 US-09-835-107-20	Sequence 20, Appl
8	158.5	93.8	31 9 US-09-835-107-21	Sequence 21, Appl
9	158.5	93.8	31 9 US-09-835-107-22	Sequence 22, Appl
10	158.5	93.8	31 9 US-09-835-107-23	Sequence 23, Appl
11	158.5	93.8	31 9 US-09-835-107-26	Sequence 26, Appl
12	158.5	93.8	31 9 US-09-835-107-27	Sequence 27, Appl
13	158.5	93.8	31 14 US-10-086-177A-13	Sequence 13, Appl

14	158.5	93.8	31 14 US-10-086-177A-15	Sequence 15, Appl
15	158.5	93.8	31 14 US-10-086-177A-20	Sequence 20, Appl
16	158.5	93.8	31 14 US-10-086-177A-21	Sequence 21, Appl
17	158.5	93.8	31 14 US-10-086-177A-22	Sequence 22, Appl
18	158.5	93.8	31 14 US-10-086-177A-23	Sequence 23, Appl
19	158.5	93.8	31 14 US-10-086-177A-26	Sequence 26, Appl
20	158.5	93.8	31 14 US-10-086-177A-27	Sequence 27, Appl
21	157.5	93.2	33 9 US-09-835-107-16	Sequence 16, Appl
22	157.5	93.2	33 9 US-09-835-107-18	Sequence 18, Appl
23	157.5	93.2	33 14 US-10-086-177A-16	Sequence 16, Appl
24	157.5	93.2	33 14 US-10-086-177A-18	Sequence 18, Appl
25	157	92.9	34 9 US-09-835-107-17	Sequence 17, Appl
26	157	92.9	34 9 US-09-835-107-19	Sequence 19, Appl
27	157	92.9	34 14 US-10-086-177A-17	Sequence 17, Appl
28	157	92.9	34 14 US-10-086-177A-19	Sequence 19, Appl
29	155.5	92.0	31 9 US-09-835-107-24	Sequence 24, Appl
30	155.5	92.0	31 9 US-09-835-107-25	Sequence 25, Appl
31	155.5	92.0	31 14 US-10-086-177A-24	Sequence 24, Appl
32	155.5	92.0	31 14 US-10-086-177A-25	Sequence 25, Appl
33	149.5	88.5	31 9 US-09-852-424-74	Sequence 74, Appl
34	149.5	88.5	31 9 US-09-852-424-122	Sequence 122, Appl
35	149.5	88.5	31 9 US-09-852-424-124	Sequence 124, Appl
36	149.5	88.5	31 9 US-09-852-424-133	Sequence 133, Appl
37	149.5	88.5	31 9 US-09-852-424-134	Sequence 134, Appl
38	149.5	88.5	31 9 US-09-852-424-135	Sequence 135, Appl
39	148	87.6	34 9 US-09-852-424-75	Sequence 75, Appl
40	148	87.6	34 9 US-09-852-424-123	Sequence 123, Appl
41	148	87.6	34 9 US-09-852-424-125	Sequence 125, Appl
42	145.5	86.1	31 9 US-09-852-424-95	Sequence 95, Appl
43	144.5	85.5	31 9 US-09-852-424-79	Sequence 79, Appl
44	144.5	85.5	31 9 US-09-852-424-94	Sequence 94, Appl
45	144	85.2	34 9 US-09-852-424-99	Sequence 99, Appl

#### ALIGNMENTS

RESULT 1  
US-09-835-107-12  
Sequence 12, Application US/09835107  
Patent No. US20020165123A1  
GENERAL INFORMATION:  
APPLICANT: Tudan, Christopher R.  
APPLICANT: Merzouk, Ahmed  
APPLICANT: Arab, Lakhdar  
APPLICANT: Saxena, Geeta  
APPLICANT: Raves, Connie J.  
APPLICANT: Cashman, Johanne  
APPLICANT: Clark-Lewis  
APPLICANT: Salari, Hassan  
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: SMAR12  
CURRENT APPLICATION NUMBER: US/09/835,107  
CURRENT FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: CA 2,305,036  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: US 60/232,425  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: CA 2,335,109  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 30  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
NAME/KEY: DOMAIN  
LOCATION: (15..(17))  
OTHER INFORMATION: spacer monomers (such as the illustrated glycine  
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3  
OTHER INFORMATION: or 4 glycines.  
OTHER INFORMATION: Synthesised in Laboratory:

OTHER INFORMATION: SDF-1(1-14) - (G)3-SDF-1(55-67) acid  
US-09-835-107-12

Query Match 100.0%; Score 169; DB 9; Length 30;  
Best Local Similarity 100.0%; Pred. No. 4.8e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGLKWIQEYLEKALN 30  
DB 1 KPVSLSYRCPCRFPGGGLKWIQEYLEKALN 30

## RESULT 2

US-09-835-107-14  
Sequence 14, Application US/09835107  
Patent No. US20020165123A1  
GENERAL INFORMATION:  
APPLICANT: Tudan, Christopher R.  
APPLICANT: Merzouk, Ahmed  
APPLICANT: Arab, Lakhdar  
APPLICANT: Saxena, Geeta  
APPLICANT: Eaves, Connie J.  
APPLICANT: Cashman, Johanne  
APPLICANT: Clark-Lewis  
APPLICANT: Salari, Hassan  
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: SMAR012  
CURRENT APPLICATION NUMBER: US/09/835,107  
CURRENT FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: CA 2,305,036  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: US 60/232,425  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: CA 2,335,109  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 30  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (15)..(17)  
OTHER INFORMATION: spacer monomers (such as the illustrated glycine  
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3  
OTHER INFORMATION: or 4 glycines.  
OTHER INFORMATION: Synthesized in Laboratory:  
NAME/KEY: MOD RES  
LOCATION: (30)  
OTHER INFORMATION: AMIDATION  
US-09-835-107-14

Query Match 100.0%; Score 169; DB 9; Length 30;  
Best Local Similarity 100.0%; Pred. No. 4.8e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGLKWIQEYLEKALN 30  
DB 1 KPVSLSYRCPCRFPGGGLKWIQEYLEKALN 30

## RESULT 3

US-10-086-177A-12  
Sequence 12, Application US/10086177A  
Publication No. US20030148940A1  
GENERAL INFORMATION:  
APPLICANT: Tudan, Christopher R.  
APPLICANT: Merzouk, Ahmed  
APPLICANT: Saxena, Geeta  
APPLICANT: Eaves, Connie J.  
APPLICANT: Cashman, Johanne

APPLICANT: Clark-Lewis, Ian  
APPLICANT: Salari, Hassan  
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic  
TITLE OF INVENTION: Cells  
FILE REFERENCE: SMAR-012CIP  
CURRENT APPLICATION NUMBER: US/10/086,177A  
CURRENT FILING DATE: 2002-02-26  
PRIOR APPLICATION NUMBER: 09/835,107  
PRIOR FILING DATE: 2001-04-12  
PRIOR APPLICATION NUMBER: 60/232,425  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: CA 2,305,036  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: CA 2,335,109  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 30  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)  
US-10-086-177A-12

Query Match 100.0%; Score 169; DB 14; Length 30;  
Best Local Similarity 100.0%; Pred. No. 4.8e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGLKWIQEYLEKALN 30  
DB 1 KPVSLSYRCPCRFPGGGLKWIQEYLEKALN 30

## RESULT 4

US-10-086-177A-14  
Sequence 14, Application US/10086177A  
Publication No. US20030148940A1  
GENERAL INFORMATION:  
APPLICANT: Tudan, Christopher R.  
APPLICANT: Merzouk, Ahmed  
APPLICANT: Saxena, Geeta  
APPLICANT: Eaves, Connie J.  
APPLICANT: Cashman, Johanne  
APPLICANT: Clark-Lewis, Ian  
APPLICANT: Salari, Hassan  
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic  
TITLE OF INVENTION: Cells  
FILE REFERENCE: SMAR-012CIP  
CURRENT APPLICATION NUMBER: US/10/086,177A  
CURRENT FILING DATE: 2002-02-26  
PRIOR APPLICATION NUMBER: 09/835,107  
PRIOR FILING DATE: 2001-04-12  
PRIOR APPLICATION NUMBER: 60/232,425  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: CA 2,305,036  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: CA 2,335,109  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 30  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)  
US-10-086-177A-14

Query Match 100.0%; Score 169; DB 14; Length 30;  
Best Local Similarity 100.0%; Pred. No. 4.8e-16;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVSLSYRCPCRFPGGGLKMIQIYLEYKALN 30  
Db 1 KPVSLSYRCPCRFPGGGLKMIQIYLEYKALN 30

## RESULT 5

US-09-835-107-13  
Sequence 13, Application US/09835107  
Patent No. US20020165123A1  
GENERAL INFORMATION:  
APPLICANT: Tudan, Christopher R.  
APPLICANT: Merzouk, Ahmed  
APPLICANT: Arab, Lakhdar  
APPLICANT: Saxena, Geeta  
APPLICANT: Bayes, Connie J.  
APPLICANT: Caehman, Johanne  
APPLICANT: Clark-Lewis  
APPLICANT: Salari, Hassan  
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: SMAR012  
CURRENT APPLICATION NUMBER: US/09/835,107  
PRIOR FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: CA 2,305,036  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: US 60/232,425  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: CA 2,335,109  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13  
LENGTH: 31  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (16)..(19)  
OTHER INFORMATION: spacer monomers (such as the illustrated glycine  
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3  
OTHER INFORMATION: Synthesised in Laboratory:  
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) acid: or CTCB0013  
US-09-835-107-13

Query Match 93.8%; Score 158.5; DB 9; Length 31;  
Best Local Similarity 96.8%; Pred. No. 1.4e-14;  
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 KPVSLSYRCPCRFPGGGLKMIQIYLEYKALN 30  
Db 1 KPVSLSYRCPCRFPGGGLKMIQIYLEYKALN 31

## RESULT 6

US-09-835-107-15  
Sequence 15, Application US/09835107  
Patent No. US20020165123A1  
GENERAL INFORMATION:  
APPLICANT: Tudan, Christopher R.  
APPLICANT: Merzouk, Ahmed  
APPLICANT: Arab, Lakhdar  
APPLICANT: Saxena, Geeta  
APPLICANT: Bayes, Connie J.  
APPLICANT: Caehman, Johanne  
APPLICANT: Clark-Lewis  
APPLICANT: Salari, Hassan  
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: SMAR012  
CURRENT APPLICATION NUMBER: US/09/835,107  
CURRENT FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: CA 2,305,036

PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: US 60/232,425  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: CA 2,335,109  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 15  
LENGTH: 31  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (15)..(18)  
OTHER INFORMATION: spacer monomers (such as the illustrated glycine  
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3  
OTHER INFORMATION: Synthesised in Laboratory:  
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) amide: or CTCB0017  
NAME/KEY: MOD RES  
LOCATION: (31)  
OTHER INFORMATION: AMIDATION  
US-09-835-107-15

Query Match 93.8%; Score 158.5; DB 9; Length 31;  
Best Local Similarity 96.8%; Pred. No. 1.4e-14;  
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 KPVSLSYRCPCRFPGGGLKMIQIYLEYKALN 30  
Db 1 KPVSLSYRCPCRFPGGGLKMIQIYLEYKALN 31

## RESULT 7

US-09-835-107-20  
Sequence 20, Application US/09835107  
Patent No. US20020165123A1  
GENERAL INFORMATION:  
APPLICANT: Tudan, Christopher R.  
APPLICANT: Merzouk, Ahmed  
APPLICANT: Arab, Lakhdar  
APPLICANT: Saxena, Geeta  
APPLICANT: Bayes, Connie J.  
APPLICANT: Caehman, Johanne  
APPLICANT: Clark-Lewis  
APPLICANT: Salari, Hassan  
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: SMAR012  
CURRENT APPLICATION NUMBER: US/09/835,107  
PRIOR FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: CA 2,305,036  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: US 60/232,425  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: CA 2,335,109  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 20  
LENGTH: 31  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (15)..(18)  
OTHER INFORMATION: spacer monomers (such as the illustrated glycine  
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3  
OTHER INFORMATION: Synthesised in Laboratory:  
OTHER INFORMATION: Cyclyzed, for example glutamate (E) and lysine (K)  
OTHER INFORMATION: residues may be joined by side chain cyclization  
OTHER INFORMATION: using a lactam formation procedure.

OTHER INFORMATION: Synthesised in Laboratory:  
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF(55-67)-B24/K28-cyclic acid  
US-09-835-107-20

Query Match 93.8%; Score 158.5; DB 9; Length 31;  
Best Local Similarity 96.8%; Pred. No. 1.4e-14;  
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KPVSLSYRCPCRF-GGGLKMIQIYLEKALN 30  
DB 1 KPVSLSYRCPCRFGGGLKMIQIYLEKALN 31

## RESULT 8

US-09-835-107-21

Sequence 21, Application US/09835107  
Patent No. US20020165123A1  
GENERAL INFORMATION:  
APPLICANT: Tuden, Christopher R.  
APPLICANT: Arab, Lakhdar  
APPLICANT: Saxena, Geeta  
APPLICANT: Eaves, Connie J.  
APPLICANT: Cashman, Johanne  
APPLICANT: Clark-Lewis  
APPLICANT: Saliari, Hassan  
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: SMAR012  
CURRENT APPLICATION NUMBER: US/09/835,107  
CURRENT FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: CA 2,305,036  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: US 60/232,425  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: CA 2,335,109  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 21  
LENGTH: 31  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (15)..(18)  
OTHER INFORMATION: spacer monomers (such as the illustrated glycine  
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3  
NAME/KEY: DOMAIN  
LOCATION: (20)..(24)  
OTHER INFORMATION: Cyclized, for example glutamate (E) and lysine (K)  
OTHER INFORMATION: residues may be joined by side chain cyclization  
OTHER INFORMATION: using a laccam formation.  
OTHER INFORMATION: Synthesised in Laboratory:  
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF(55-67)-K20/B24-cyclic acid  
US-09-835-107-21

Query Match 93.8%; Score 158.5; DB 9; Length 31;  
Best Local Similarity 96.8%; Pred. No. 1.4e-14;  
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KPVSLSYRCPCRF-GGGLKMIQIYLEKALN 30  
DB 1 KPVSLSYRCPCRFGGGLKMIQIYLEKALN 31

## RESULT 9

US-09-835-107-22

Sequence 22, Application US/09835107  
Patent No. US20020165123A1  
GENERAL INFORMATION:  
APPLICANT: Tuden, Christopher R.  
APPLICANT: Merzouk, Ahmed

APPLICANT: Arab, Lakhdar  
APPLICANT: Saxena, Geeta  
APPLICANT: Eaves, Connie J.  
APPLICANT: Cashman, Johanne  
APPLICANT: Clark-Lewis  
APPLICANT: Saliari, Hassan  
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: SMAR012  
CURRENT APPLICATION NUMBER: US/09/835,107  
CURRENT FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: CA 2,305,036  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: US 60/232,425  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: CA 2,335,109  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 22  
LENGTH: 31  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (15)..(18)  
OTHER INFORMATION: spacer monomers (such as the illustrated glycine  
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3  
OTHER INFORMATION: or 4 glycines.  
NAME/KEY: DOMAIN  
LOCATION: (24)..(28)  
OTHER INFORMATION: Cyclized, for example (E) and lysine (K) residues  
OTHER INFORMATION: may be joined by side chain cyclization using a  
OTHER INFORMATION: laccam formation procedure.  
OTHER INFORMATION: Synthesised in Laboratory:  
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF(55-67)-B24/K28-cyclic  
OTHER INFORMATION: amide: or CTC80022  
NAME/KEY: MOD RES  
LOCATION: (31)  
OTHER INFORMATION: AMIDATION  
US-09-835-107-22

Query Match 93.8%; Score 158.5; DB 9; Length 31;  
Best Local Similarity 96.8%; Pred. No. 1.4e-14;  
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KPVSLSYRCPCRF-GGGLKMIQIYLEKALN 30  
DB 1 KPVSLSYRCPCRFGGGLKMIQIYLEKALN 31

## RESULT 10

US-09-835-107-23

Sequence 23, Application US/09835107  
Patent No. US20020165123A1  
GENERAL INFORMATION:  
APPLICANT: Tuden, Christopher R.  
APPLICANT: Arab, Lakhdar  
APPLICANT: Saxena, Geeta  
APPLICANT: Eaves, Connie J.  
APPLICANT: Cashman, Johanne  
APPLICANT: Clark-Lewis  
APPLICANT: Saliari, Hassan  
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: SMAR012  
CURRENT APPLICATION NUMBER: US/09/835,107  
CURRENT FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: CA 2,305,036  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: US 60/232,425  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: CA 2,335,109  
PRIOR FILING DATE: 2001-02-23

```

; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (15)..(18)
; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
; OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
; OTHER INFORMATION: or 4 glycines.
; NAME/KEY: DOMAIN
; LOCATION: (20)..(24)
; OTHER INFORMATION: Cylcyclized, for example glutamate (E) and lysine
; OTHER INFORMATION: (K) residues may be joined by side chain
; OTHER INFORMATION: cyclization using a lactam formation procedure.
; OTHER INFORMATION: Synthesised in Laboratory:
; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/E24-cyclic
; NAME/KEY: MOD_RES
; LOCATION: (31)
; OTHER INFORMATION: amide: or CTCB0021
US-09-835-107-23

Query Match          93.8%; Score 158.5; DB 9; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1 KPVSLSYRCPCRF-GGGLKMWIOEYLEKALN 30
Db      1 KPVSLSYRCPCRFGGGGLKMWIOEYLEKALN 31

RESULT 11
US-09-835-107-26
; Sequence 26, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (15)..(18)
; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
; OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
; OTHER INFORMATION: or 4 glycines.
; NAME/KEY: DISULFID
; LOCATION: (9)..(11)
; OTHER INFORMATION: cysteine residues may for example be involved in
; OTHER INFORMATION: bridge formation
```

```

; OTHER INFORMATION: Synthesised in Laboratory:
; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-C9/C11-cyclic acid
US-09-835-107-26

Query Match          93.8%; Score 158.5; DB 9; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1 KPVSLSYRCPCRF-GGGLKMWIOEYLEKALN 30
Db      1 KPVSLSYRCPCRFGGGGLKMWIOEYLEKALN 31

RESULT 12
US-09-835-107-27
; Sequence 27, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (15)..(18)
; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
; OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
; OTHER INFORMATION: or 4 glycines.
; NAME/KEY: DISULFID
; LOCATION: (9)..(11)
; OTHER INFORMATION: Cysteine residues may for example be involved in
; OTHER INFORMATION: bridge formation.
; OTHER INFORMATION: Synthesised in Laboratory:
; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-C9/C11-cyclic amide
; NAME/KEY: MOD_RES
; LOCATION: (31)
; OTHER INFORMATION: AMIDATION
US-09-835-107-27

Query Match          93.8%; Score 158.5; DB 9; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1 KPVSLSYRCPCRF-GGGLKMWIOEYLEKALN 30
Db      1 KPVSLSYRCPCRFGGGGLKMWIOEYLEKALN 31

RESULT 13
US-10-086-177A-13
; Sequence 13, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
```

```
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Saxena, Geeta
APPLICANT: Bayes, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
FILE REFERENCE: SMAR-012CIP
CURRENT APPLICATION NUMBER: US/10/086,177A
PRIOR FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
US-10-086-177A-13

Query Match          93.8%; Score 158.5; DB 14; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Cy 1 KPVSLSTRCPGRPF-GGGLKMIQIYLEKALN 30
Db 1 KPVSLSTRCPGRPFGGGLKMIQIYLEKALN 31

RESULT 14
US-10-086-177A-15
Sequence 15, Application US/10086177A
Publication No. US20030148940A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Saxena, Geeta
APPLICANT: Bayes, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
FILE REFERENCE: SMAR-012CIP
CURRENT APPLICATION NUMBER: US/10/086,177A
PRIOR FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
```

```
OTHER INFORMATION: 3-SDF-1 (55-67) amide: or CTCB0017
US-10-086-177A-15

Query Match          93.8%; Score 158.5; DB 14; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Cy 1 KPVSLSTRCPGRPF-GGGLKMIQIYLEKALN 30
Db 1 KPVSLSTRCPGRPFGGGLKMIQIYLEKALN 31

RESULT 15
US-10-086-177A-20
Sequence 20, Application US/10086177A
Publication No. US20030148940A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Saxena, Geeta
APPLICANT: Bayes, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
FILE REFERENCE: SMAR-012CIP
CURRENT APPLICATION NUMBER: US/10/086,177A
PRIOR FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
US-10-086-177A-20

Query Match          93.8%; Score 158.5; DB 14; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Cy 1 KPVSLSTRCPGRPF-GGGLKMIQIYLEKALN 30
Db 1 KPVSLSTRCPGRPFGGGLKMIQIYLEKALN 31

Search completed: January 4, 2005, 16:04:59
Job time : 97.8689 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 4, 2005, 15:43:59 ; Search time 12.2951 Seconds  
(without alignments)  
234.769 Million cell updates/sec

Title: US-10-086-177A-12

Perfect score: 169  
Sequence: 1 KPVSLSYRCPCRFPGGGLKMWIKYLEKALN 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118.5	70.1	89	2	153416 interluekin-8 homo
2	118.5	70.1	89	2	A53497 pre-B-cell growth-
3	118.5	70.1	93	2	G01540 cytokine SDF-1-beta
4	118.5	70.1	93	2	181182 cytokine - mouse
5	59.5	35.2	1084	2	T08583 cellulose synthase
6	59.5	35.2	1088	2	H84604 probable cellulose
7	56.5	33.4	1081	2	152028 cellulose synthase
8	54.5	32.2	233	2	T35594 hypothetical prote
9	54.5	32.2	1400	2	T22644 cellulose synthase
10	52	30.8	974	2	T10797 cellulose synthase
11	50.5	29.9	3433	1	GNMVKV genome polypeptid
12	49.5	29.3	189	2	D63389 DNA-directed RNA p
13	49.5	29.3	469	2	C63345 probable class III
14	49.5	29.3	556	1	A53376 tryptophan 2-monoo
15	49.5	29.3	557	1	A25493 catechol oxidase f
16	49.5	29.3	588	2	S34786 ADP-ribosylation f
17	49.5	29.3	1147	2	T42627 probable RNA-bind
18	49	29.0	347	2	T15147 probable RNA-bind
19	49	29.0	347	2	I15146 hypothetical RNA-b
20	49	29.0	439	2	E72288 hypothetical prote
21	49	29.0	577	2	I50731 Ig heavy chain - n
22	48.5	28.7	685	2	T10800 cellulose synthase
23	48.5	28.7	1429	2	S06434 homeoic protein 1
24	48	28.4	312	2	T23493 hypothetical prote
25	48	28.4	340	2	T23492 hypothetical prote
26	47.5	28.1	212	2	G73466 probable alpha-1,2
27	47.5	28.1	318	2	T11713 probable RNA polym
28	47	27.8	311	2	H71252 acetate kinase ack
29	47	27.8	390	2	S73635

30	47	27.8	402	2	T14438 phosphate/triose-p
31	47	27.8	618	2	T00476 probable vacuolar
32	47	27.8	805	2	A69682 primosomal replica
33	47	27.8	1008	2	T30544 major surface glyc
34	46.5	27.5	431	2	T29716 hypothetical prote
35	46.5	27.5	470	2	T46814 gamma-aminobutyrat
36	46.5	27.5	470	2	B95419 diaminobutyrate-py
37	46.5	27.5	548	2	E72457 probable phenylala
38	46	27.2	122	2	T45165 succinate dehydrog
39	46	27.2	161	2	B84366 hypothetical prote
40	46	27.2	247	2	T02393 hypothetical prote
41	46	27.2	262	2	B95289 hypothetical prote
42	46	27.2	379	2	T06610 hypothetical prote
43	46	27.2	393	2	E64239 acetate kinase (BC
44	46	27.2	804	2	E83963 primosomal replica
45	46	27.2	1017	2	T08553 hypothetical prote

#### ALIGNMENTS

```

RESULT 1
153416
interluekin-8 homolog - mouse
C:Species: Mus sp. (mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: 153416
R:Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.
Exp. Cell Res. 215, 284-293, 1994
A:Title: Molecular cloning of TP41, a gene whose expression is repressed by the tumor
A:Reference number: 153416; MUID:95073497; PMID:7982471
A:Accession: 153416
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89 <RES>
A:Cross-references: GB:574318; NID:9786393; PIDN:AAB32650.1; PID:9786394
C:Genetics:
A:Gene: TP41
C:Superfamily: beta-chromoglobulin

Query Match          70.1%; Score 118.5; DB 2; Length 89;
Best Local Similarity 40.3%; Pred. No. 3.5e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFPGG-----GLKWIQZ 23
   |||||
Db 22 KPVSLSYRCPCRFPGGSHIARAVYHKLINTPNCALQIVARLKNRQVCIDPGLKWIQZ 81
   |||||

QY 24 YLEKALN 30
   |||||
Db 82 YLEKALN 88

RESULT 2
A53497
pre-B-cell growth-stimulating factor precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004
C:Accession: A53497; I59582
R:Nagasawa, T.; Kikutani, H.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994
A:Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.
A:Reference number: A53497; MUID:94181581; PMID:8134392
A:Accession: A53497
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-89 <NAG>
A:Cross-references: UNIPROT:P40224; GB:D21072; NID:g413905; PIDN:BAA04648.1; PID:g46845
R:Ishino, K.; Tada, H.; Heller, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I memb
A:Reference number: I59582; MUID:93342488; PMID:8342023
A:Accession: I59582

```

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-89 <RES>  
A:Cross-references: GB:IL12029, NID:G393179, PIDN:AAA40100.1, PID:G393180  
C:Gene: SDP-1- $\alpha$ pha  
C:Superfamily: beta-Chromoglobulin  
C:Keywords: cytokine

Query Match	70.1%;	Score 118.5;	DB 2;	Length 89;
Best Local Similarity	40.3%;	Pred. No. 3.5e-09;		
Matches	27;	Conservative	0;	Mismatches 3;
				Indels 37;
				Gaps 1;

RESULT 3  
G01540  
Cytokine SDF-1-beta - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1996 #sequence\_rev1sion 06-Jun-1997 #next\_change 09-Jul-2004  
A:Accession: G01540  
R:Spotlta, L.D.  
submitted to the EMBL Data Library, October 1994  
A:Reference number: G07697  
A:Accession: G01540  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-93 <6PO>  
A:Cross-references: UNIRROT:P48061; EMBL:U16752; NID:g1272194; PTD:G571508  
A:Superfamily: beta-Chromoglobulin

Query Match	70.1%;	Score 118.5;	DB 2;	Length 93;
Best Local Similarity	40.3%;	Pred. No. 3.6e-09;		
Matches 27; Conservative	0;	Mismatches 3;	Indels 37;	Gaps 1.

RESULT 4  
181182 cytokine - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: 181182  
R:Tashiro, K., Tada, H., Heikler, R., Shirozu, M., Nakano, T., Honjo, T.  
Science 261, 600-603, 1993  
A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I mem  
A:Reference number: 159582; PMID:93342488; PMID:8342023  
A:Accession: 181182  
A:Structure: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-93 <RES>  
A:Cross-references: UNIPROT:P40224; GB:LI2030; NID:G393181; PTDN:AAA40101.1; PID:G393182  
C:Genetic:ca  
A:Gene: SDR-1-beta  
C:Superfamily: beta-thromboglobulin

Query Match	70.1%	Score 118.5	DB 2	Length 93
Best Local Similarity	40.3%	Pred. No. 3.6e-09		
Matches 27; Conservative	0	Mismatches 3	Indels 37	Gaps 1

Oy		1	KPVSLSRCCRFEEGG-----GLKXIOE	23
Dd		22	KPVSLSYRCPCRFESHIAADANVGHKLINTPNCAIQIVARLGNRRQVCIDPKLKMOE	81
Oy		24	YLKKALN	30
Dd		82	YLEKAALN	88

RESULT 5  
T08563  
cellulose synthase (EC 2.4.1.-) catalytic chain - Arabidopsis thaliana  
N/Alternate names: protein T22F8.250  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C/Accession: T08563; T09014  
R/Beyan, M.; Zimmermann, W.; Gruenleisen, A.; Wandut, R.; Bancroft, I.; Mewes, H.W.; May  
submitted to the Protein Sequence Database, May 1999  
A/Reference number: Z16442

Query Match	35.2%	Score 59.5	DB 2	Length 1084
Best Local Similarity	43.5%	Pred. No. 4.1		
Matches	10	Conservative	6	Mismatches 6; Indels 1; Gaps 1
QY	3	VSLSYRCPGR-FGGGLKMIQDY	24	
DB	833	IFLSRHCPIMYGCGGLKMLERF	855	

RESULT 6  
 H84604  
 Probable cellulose synthase catalytic subunit [imported] - *Arabidopsis thaliana*  
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
 C/Accession: H84604  
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Banfic, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhaken, S.B.; Umayam, L.; Tallon, L.  
 euse, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
 Nature 402, 761-768, 1999  
 A/TITLE: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
 A/Reference number: A84420; MUID:20083487; PMID:10617197

Query Match	Score	DB 2;	Length
Best Local Similarity	43.5%;	Pred. No. 4.1;	1088;

Matches 10; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 3 VSLSYRCPCRF-FGGGLKMIQ 24

Db 837 IFLSRHCPIMWYGGLKMIERF 859

#### RESULT 7

T52028 cellulose synthase [imported] - Arabidopsis thaliana (fragment)

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004

C/Accession: T52028

R/Joshi, C.

submitted to the EMBL Data Library, May 1998

A/Reference number: Z25890

A/Accession: T52028

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1081 <JOS>

A/Cross-references: UNIPROT:O65338; EMBL:AF062485; PIDN:AA029067.1

Query Match 33.4%; Score 56.5; DB 2; Length 1081;  
Best Local Similarity 47.6%; Pred. No. 11;  
Matches 10; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 3 VSLSYRCPCRF-FGGGLKMIQ 22

Db 831 IFLSRHCPIMWYGGLKMLE 851

#### RESULT 8

T35594 hypothetical protein SC6G4.43c SC6G4.43c - Streptomyces coelicolor

C/Species: Streptomyces coelicolor

C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004

C/Accession: T35594

R/Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1998

A/Reference number: Z21583

A/Accession: T35594

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-233 <SAU>

A/Cross-references: UNIPROT:O68604; EMBL:AL031317; PIDN:CAA20421.1; GSPDB:GN00070; SCOP

A/Experimental source: strain A3(2)

C/Genetics:

A/Gene: SC6DB:SC6G4.43c

C/Superfamily: hypothetical protein H10278

Query Match 32.2%; Score 54.5; DB 2; Length 233;  
Best Local Similarity 40.0%; Pred. No. 5.1;  
Matches 10; Conservative 6; Mismatches 6; Indels 3; Gaps 1;

QY 6 SYRCPFRFGGL---KMIQVLEK 27

Db 135 SGRIPCRFQGHGMBPRVWKRPMK 159

#### RESULT 9

T22644 hypothetical protein F54D1.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T22644

R/Lemard, N.

submitted to the EMBL Data Library, July 1996

A/Reference number: Z19592

A/Accession: T22644

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1400 <WLU>

A/Cross-references: UNIPROT:Q20766; EMBL:Z77132; PIDN:CAB00861.1; GSPDB:GN00022; CESP:FS

A/Experimental source: clone F54D1

C/Genetics:

A/Gene: CESP:F54D1.5

A/Map position: 4

A/Intons: 21/2; 51/2; 205/2; 276/3; 364/2; 394/2; 466/3; 507/3; 536/3; 599/3; 672/2; 6

Query Match 32.2%; Score 54.5; DB 2; Length 1400;  
Best Local Similarity 42.9%; Pred. No. 25;  
Matches 12; Conservative 3; Mismatches 10; Indels 3; Gaps 1;

QY 3 VSLSYRCPCRF-FGGGLKMIQVLEKALN 30

Db 476 VDLAKSC--LFGNGRKMSSDVLEKAMN 500

#### RESULT 10

T10797 cellulose synthase (EC 2.4.1.-) catalytic chain celA1 - upland cotton

C/Species: Gossypium hirsutum (upland cotton)

C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C/Accession: T10797

R/Pear, J.R.; Kawagoe, Y.; Schreckengost, W.E.; Delmer, D.P.; Stalker, D.M.

Proc. Natl. Acad. Sci. U.S.A. 93, 12637-12642, 1996

A/Title: Higher plants contain homologs of the bacterial celA genes encoding the cataly

A/Reference number: Z17152; MUID:97057296; PMID:891635

A/Accession: T10797

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-974 <PEA>

A/Cross-references: UNIPROT:P91155; EMBL:U58283; NID:G1706955; PIDN:AB37766.1; PID:G17

A/Experimental source: strain Acala S2-2; fiber

C/Genetics:

A/Gene: celA1

C/Function:

A/Description: involved in the synthesis of cellulose

C/Keywords: glycosyltransferase; hexosyltransferase

Query Match 30.8%; Score 52; DB 2; Length 974;  
Best Local Similarity 54.5%; Pred. No. 40;  
Matches 12; Conservative 3; Mismatches 5; Indels 2; Gaps 2;

QY 3 VSLSYRCPCRF-FGGGLKMIQ 22

Db 721 IFLSRHCPIMWYGGLKMIQ 742

#### RESULT 11

GNMYKV genome polyprotein - Kunjin virus (strain MEM61C)

N/Contains: capsid protein C; envelope protein E; membrane protein M; nonstructural pro

in NS4a; nonstructural protein NS4b; nonstructural protein NS5

C/Species: Kunjin virus

C/Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-Jul-2004

C/Accession: A28697

R/Cola, G.; Parker, M.D.; Speight, G.; Byrne, M.E.; Westaway, E.G.

J. Gen. Virol. 69, 1-21, 1988

A/Title: Nucleotide and complete amino acid sequences of Kunjin virus: definitive gene

A/Reference number: A28697; MUID:88089524; PMID:2826559

A/Accession: A28697

A/Molecule type: genomic RNA

A/Residues: 1-3433 <COI>

A/Cross-references: UNIPROT:P14335; GB:D00246; NID:G221966; PIDN:BAA00176.1; PID:G22196

C/Superfamily: yellow fever virus genome polyprotein

C/Keywords: ATP; capsid protein; envelope protein; membrane protein; nonstructural prot

F/2-123/Product: capsid protein C #status predicted <CPC>

F/124-290/Product: membrane protein M precursor #status predicted <MP>

F/124-215/Domain: nonterminal signal sequence #status predicted <SIG>

F/216-280/Product: membrane protein M #status predicted <MP>

F/291-791/Product: envelope protein B #status predicted <EP>

F/792-1143/Product: nonstructural protein NS1 #status predicted <NS1>

F/1144-1374/Product: nonstructural protein NS2a #status predicted <NS2a>

F/1375-1505/Product: nonstructural protein NS2b #status predicted <NS2b>

F/1506-2124/Product: nonstructural protein NS3 #status predicted <NS3>

F:1699-1706/Region: nucleotide-binding motif A (P-loop)

F:1786-1793/Region: nucleotide-binding motif B

F:1790-1793/Region: DBA motif

F:2125-2273/Product: nonstructural protein NS4a #status predicted <NA>

F:2274-2528/Product: nonstructural protein NS4b #status predicted <NA>

F:2529-3433/Product: nonstructural protein NS5 #status predicted <NS5>

Query Match 29.9% Score 50.5; DB 1; Length 3433;

Best Local Similarity 37.9%; Pred. No. 2e+02;

Matches 11; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

Db 2 PVS-LSYRCPCRFPGGGLKWIQVLEKAL 29

1837 PISDLQTEIPDRANWNGVEMTEYIGKTV 1865

#### RESULT 12

D69389

DNA-directed RNA polymerase, subunit E' (rpoB1) homolog - Archaeoglobus fulgidus

C/Species: Archaeoglobus fulgidus

C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004

C/Accession: D69389

R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A/Authors: Ueberbach, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea

A/Reference number: A69250; MUID:98049343; PMID:9389475

A/Accession: D69389

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-189 <KLE>

A/Cross-references: UNIPROT:O29148; GB:AE001027; GB:AE000782; NID:92689350; PTDN:AA9012

C/Superfamily: DNA-directed RNA polymerase subunit E

Query Match 29.3% Score 49.5; DB 2; Length 189;

Best Local Similarity 40.7%; Pred. No. 21;

Matches 11; Conservative 6; Mismatches 7; Indels 3; Gaps 1;

Db 3 VSLSYRCPCRFPGGGLKWIQVLEKAL 29

161 IGLTRQP---WLGALKWIEEIEKLM 184

#### RESULT 13

C83345

Probable class III aminotransferase PA2413 [imported] - Pseudomonas aeruginosa (strain F

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004

C/Accession: C83345

R/Sover, C.K.; Pham, X.Q.; Eryin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.

adman, S.; Yun, Y.; Brody, L.V.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,

.; Loay, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: C83345

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-469 <STO>

A/Cross-references: UNIPROT:Q91168; GB:AE004668; GB:AE004091; NID:99948446; PTDN:AA0580

C/Experimental source: strain PA01

C/Genetics:

A/Gene: PA2413

Query Match 29.3% Score 49.5; DB 2; Length 469;

Best Local Similarity 43.3%; Pred. No. 46;

Matches 13; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

Db 2 PVSLSYRCPCRFPGGGLKWIQVLEKAL 30

1 PVSLSYRCPCRFPGGGLKWIQVLEKAL 30

#### RESULT 14

A53376

Cryptophan 2-monooxygenase (EC 1.13.12.3) - Pseudomonas syringae pv. syringae

C/Species: Pseudomonas syringae pv. syringae

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C/Accession: A53376

R/Mazzola, M.; White, F.F.

J. Bacteriol. 176, 1374-1382, 1994

A/Title: A mutation in the indole-3-acetic acid biosynthesis pathway of Pseudomonas syri

A/Reference number: A53376; MUID:94156842; PMID:8113177

A/Accession: A53376

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-556 <MAZ>

Db 199 PYPDYRCPEGLGEGAVKANLHYLENLN 228

#### RESULT 15

A25493

Cryptophan 2-monooxygenase (EC 1.13.12.3) - Pseudomonas syringae pv. savastanoi

C/Species: Pseudomonas syringae pv. savastanoi

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C/Accession: A25493

R/Yamada, T.; Palm, C.J.; Brooks, B.; Koenig, T.

Proc. Natl. Acad. Sci. U.S.A. 82, 6522-6526, 1985

A/Title: Nucleotide sequences of the Pseudomonas savastanoi indoleacetic acid genes sho

A/Reference number: A94062

A/Accession: A25493

A/Molecule type: DNA

A/Residues: 1-557 <YAM>

A/Cross-references: UNIPROT:P06617

C/Genetics:

A/Gene: laam

C/Superfamily: Pseudomonas cryptophan 2-monooxygenase

C/Keywords: monooxygenase; oxidoreductase

Query Match 29.3% Score 49.5; DB 1; Length 556;

Best Local Similarity 45.5%; Pred. No. 53;

Matches 10; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

Db 9 CPGRFPGGGLKWIQVLEKALN 30

510 CSCSPFAGG---WIEGAVQTALN 528

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

511 CSCSPFAGG---WIEGAVQTALN 529

Search completed: January 4, 2005, 15:44:32

Job time: 13.2951 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 4, 2005, 15:43:59 ; Search time 57.541 Seconds  
(without alignments)  
299.982 Million cell updates/sec

Title: US-10-086-177A-12

Perfect score: 169  
Sequence: 1 KPVSLSYRCPCRFPGSLKWIQVLEKALN 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_tramb1:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118.5	70.1	89	1 SDF1_MOUSE	P40224 mus musculus
2	118.5	70.1	89	2 Q8HYD0	Q8HYD0 macaca mulatta
3	118.5	70.1	89	2 BA28601	BA28601 felis sil
4	118.5	70.1	89	2 CAC10203	CAC10203 homo sapi
5	118.5	70.1	89	2 BAC32216	BAC32216 mus muscu
6	118.5	70.1	89	2 BAC35845	BAC35845 mus muscu
7	118.5	70.1	89	2 CAG29279	CAG29279 homo sapi
8	118.5	70.1	92	2 Q9H554	Q9H554 homo sapien
9	118.5	70.1	93	1 SDF1_FELCA	O62657 felis silve
10	118.5	70.1	116	1 SDF1_HUMAN	P40601 homo sapien
11	118.5	70.1	137	2 Q6EKW4	Q6EKW4 sus scrofa
12	118.5	70.1	89	2 Q6T7C0	Q6T7C0 mus musculu
13	117.5	69.5	89	2 AAR88102	AAR88102 gallus gall
14	117.5	69.5	89	2 AAR91695	AAR91695 gallus ga
15	117.5	69.5	131	2 AAR91696	AAR91696 gallus gall
16	117.5	69.5	89	2 Q9OZD1	Q9OZD1 rattus norv
17	117.5	68.3	89	2 Q80YV8	Q80YV8 rattus norv
18	115.5	68.3	119	2 Q80YV8	Q80YV8 rattus norv
19	115.5	68.3	94	2 Q80YV8	Q80YV8 xenopus lae
20	108.5	64.2	94	2 AAH61945	AAH61945 xenopus l
21	108.5	64.2	507	2 Q93YB8	Q93YB8 arabidopsis
22	59.5	35.2	1084	2 Q48947	Q48947 arabidopsis
23	59.5	35.2	1088	2 Q9SJ22	Q9SJ22 arabidopsis
24	59.5	35.2	97	2 Q6V9B5	Q6V9B5 brachydanio
25	59	34.9	97	2 AAQ24225	AAQ24225 brachydan
26	59	34.9	192	2 Q707H1	Q707H1 escherichia
27	57.5	34.0	192	2 CAE85184	CAE85184 escherich
28	57.5	34.0	192	2 Q7C009	Q7C009 shigella fl
29	57.5	34.0	199	2 Q83J00	Q83J00 shigella fl
30	57.5	34.0	199	2 Q8PKT6	Q8PKT6 escherichia
31	57.5	34.0	199	2 Q8PKT6	Q8PKT6 escherichia

32	57.5	34.0	1078	2 Q6UDP1	Q6UDP1 zea mays (m
33	57.5	34.0	1078	2 AAR23310	AAR23310 zea mays
34	57.5	34.0	1084	2 Q6UG06	Q6UG06 pinus radia
35	57	33.7	99	2 Q8AV10	Q8AV10 brachydanio
36	57	33.7	99	2 AAS92649	AAS92649 brachydan
37	57	33.7	424	2 Q9VCS4	Q9VCS4 drosophila
38	56.5	33.4	293	2 Q7VB23	Q7VB23 prochloroco
39	56.5	33.4	346	2 Q8L778	Q8L778 arabidopsis
40	56.5	33.4	366	2 Q94U06	Q94U06 arabidopsis
41	56.5	33.4	1069	2 Q9F1B9	Q9F1B9 arabidopsis
42	56.5	33.4	1081	2 Q65338	Q65338 arabidopsis
43	56.5	33.4	1084	2 Q9FGF9	Q9FGF9 arabidopsis
44	56.5	33.4	1087	2 Q6XCZ2	Q6XCZ2 populus tre
45	56.5	33.4	1087	2 AAP40636	AAP40636 populus t

## ALIGNMENTS

RESULT 1	SDF1_MOUSE	STANDARD;	PRT;	89 AA.
AC	P40224;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (pre-B cell growth stimulating factor) (PBSF) (12-O-tetradecanoylphorbol 13-acetate repressed protein 1) (TPAR1) (Thymic lymphoma cell stimulating factor) (TISF).			
DE	factor) (TISF).			
GN	Name=Cxcl12; Synonyms=Sdf1;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	Medline=94181581; PubMed=8134392;			
RA	Nagaesawa T., Kikuchi H., Kishimoto T.;			
RT	"Molecular cloning and structure of a pre-B-cell growth-stimulating factor.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	Medline=93342486; PubMed=8342023; Shirozu M., Nakano T., Honjo T.;			
RA	Tashiro K., Tada H., Heilker R.;			
RT	"Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins.";			
RL	Science 261:600-603(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	Medline=95073497; PubMed=7982471;			
RA	Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D., Weinstein I.B.;			
RT	"Molecular cloning of TPARI, a gene whose expression is repressed by the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).";			
RL	Exp. Cell Res. 215:284-293(1994).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	STRAIN=AKR/J;			
RA	Nomura M., Nakata Y., Uzawa A., Nose M., Akashi M., Suzuki G.;			
RT	Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.			
RL	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	STRAIN=C57BL/6J; TISSUE=Kidney;			
RA	Medline=22354683; PubMed=12466851; DOI=10.1038/nature01266;			
RT	Ozekati Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.;			
RL	Nakada I., Oseko N., Saito R., Suzuki H., Yamanka I., Kiyosawa H.;			
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.;			
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.;			
RA	Schirral L.M., Kanapin A., Matsuda H., Batalov S., Betzel K.W.;			
RA	Blake J.A., Bradt D., Brusci V., Chochia C., Corbani L.E., Cousins S.;			
RA	Dalla B., Dregani T.A., Fletcher C.F., Forrest A., Frazer K.S.;			
RA	Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.;			

RA Grimmond S., Guetlinch S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konegaya A., Kurochko I.V., Lee Y., Lennhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numa K., Okido T., Pavan W.J., Petrea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramachandran S.,  
RA Ravaei T., Reed J.C., Reed D.J., Reid J., Ring B., Ringwald M.,  
RA Sanderlin A., Schneider C., Sempke C.A., Setou M., Shmada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Vetraro R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilmig L.G., Wyszynski-Boris A., Yangilewa M., Yang L., Yang L.,  
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shiragawa A.,  
RA Yamanishi A., Yoshino M., Waterson R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs".  
RL Nature 420:563-573(2002).  
RL  
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
RC STRAIN=CS7BL/6J; TISSUE=Mammary gland;  
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datcchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stempelson M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshlyuk S., Carninci P., Prange C.,  
RA Bates S.S., Loguailano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Rosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
RA Schermer A., Schein J.B., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: Chemottractant active on T-lymphocytes, monocytes, but  
CC not neutrophils.  
CC -1- FUNCTION: Stimulates the proliferation of bone marrow-derived b  
CC progenitor cells in the presence of IL-7 as well as growth of the  
CC stromal cell-dependent B-cell clone DM34 cells.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named Isoform=2;  
CC Name=Alpha;  
CC IsoId=P40224-1; Sequence=Displayed;  
CC Name=Beta;  
CC IsoId=P40224-2; Sequence=VSP\_001057;  
CC -1- SIMILARITY: Belongs to the Interleukin alpha (chemokine CXC)  
CC family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-ebi.ch](mailto:license@isb-ebi.ch)).  
CC -----  
CC EMBL; D21072; BAA04648.1; -  
CC EMBL; L12029; AAA040100.1; -  
CC DR EMBL; L12030; AAA040101.1; -  
CC DR EMBL; S74318; AAB32650.1; -  
CC EMBL; D43804; BAA07862.1; -

DR EMBL; D43805; BAA07863.1; -  
DR EMBL; AK075596; BAC35845.1; -  
DR EMBL; BC006640; AAB06640.1; -  
DR PIR; A53497; A53497.  
DR PIR; I81182; I81182.  
DR HSSP; P48061; ISDF.  
DR MGI; MGI:103556; Cxcl12.  
DR GO; GO:0008009; F:chemokine activity; IDA.  
DR GO; GO:0007420; P:brain development; IDA.  
DR GO; GO:0030334; P:regulation of cell migration; IDA.  
DR GO; GO:0042098; P:T-cell proliferation; IMP.  
DR InterPro; IPR002473; C-X-C/Interlkn.8.  
DR InterPro; IPR001811; Chemokine IL8.  
DR InterPro; IPR001089; CXC\_chemkine\_sm1.  
DR Pfam; PF00048; IL8; 1.  
DR PRINTS; PR00436; INTERLEUKIN8.  
DR PROSITE; PS00471; SMALL\_CYTOKINES\_CXC; FALSE NEG.  
DR Alternative splicing; Chemotaxis; Cytokine; Growth factor; Signal.  
KW SIGNAL 1 21 Potential.  
FT CHAIN 22 89 Stromal cell-derived factor 1.  
FT DISULFID 30 55 By similarity.  
FT DISULFID 32 71 By similarity.  
FT VARSPIC 89 89 K->R(LKM (in isoform Beta).  
FT FTId=VSP\_001057.  
SQ SEQUENCE 89 AA; 10032 MW; C48BAD69078B55F5A CRC64;  
Query Match 70.1%; Score 118.5; DB 1; Length 89;  
Best Local Similarity 40.3%; Pred. No. 1.3e-09;  
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;  
QY 1 KPVSLSYRCRCRPFEGG-----GLKWIQF 23  
Db 22 KPVSLSYRCRCRPFESHIANVYKHILINTPACIQIVARLKNRRQVCIDPKLKWIOE 81  
QY 24 YLEKALN 30  
Db 82 YLEKALN 88  
RESULT 2  
ID 08HYPO PRELIMINARY; PRT; 89 AA.  
AC 08HYPO;  
DT 01-MAR-2003 (TEMBREL. 23, Created)  
DT 01-MAR-2003 (TEMBREL. 23, Last sequence update)  
DT 01-JUN-2003 (TEMBREL. 24, Last annotation update)  
DE Chemokine CXCL12/SDF-1ALPHA.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2213042; PubMed=12126650;  
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;  
RT "Molecular cloning and sequencing of 25 different rhesus macaque  
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CXC,  
RT AND CXC3C families of chemokines".  
RL Cytokine 18:140-148(2002).  
RL EMBL; AF449283; AAN76086.1; -  
DR HSSP; P48061; ISDF.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0008009; F:chemokine activity; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR002473; C-X-C/Interlkn.8.  
DR InterPro; IPR001811; Chemokine IL8.  
DR Pfam; PF00048; IL8; 1.  
DR PRINTS; PR00436; INTERLEUKIN8.  
DR SMART; SM00199; SCY; 1.  
SQ SEQUENCE 89 AA; 10105 MW; AD531633C6DC2B07 CRC64;  
Query Match 70.1%; Score 118.5; DB 2; Length 89;

SEQ	SEQUENCE	AA:	10103	MW:	62B44E8D209C3A14	CRC64:
1	NON-CLN	1	1			

RT sequencing pipeline with 384 multicapillary sequencer." /

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RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RA Adachi U., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kohjiya Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Nomazaki R., Ohno M., Ohnato N., Okazaki Y.,
RA Saito K., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RA Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AK045092; BAC32216.1; -. C4B8AD69078B55FA CRC64;
SQ SEQUENCE 89 AA; 10032 MW; C4B8AD69078B55FA CRC64;

Query Match 70.1%; Score 118.5; DB 2; Length 89;
Best Local Similarity 40.3%; Pred. No. 1.3e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSTRCPGCRFFG-----GLKRIQ 23
    |||||
DB 22 KPVSLSTRCPGFESHIRANVXHLKINTPNCALQIVARLKNRNQVCIDPKLXWIOE 81
    |||||
QY 24 YLEKALN 30
    |||||
DB 82 YLEKALN 88

RESULT 6
BAC35845 PRELIMINARY; PRT; 89 AA.
AC BAC35845;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE Adult male kidney cDNA, RIKEN full-length enriched library,
DE clone:0610039H13 product:stromal cell derived factor 1, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA MEDLINE=20493374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

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RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama U., Nishi K., Kitesunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Macanusa S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA Adachi U., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arikawa T., Bono H., Carninci P., Fukuda S., Furunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kohjiya Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yamanaka I., Yasunishi A.,
RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
RA Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AK075596; BAC35845.1; -. C4B8AD69078B55FA CRC64;
SQ SEQUENCE 89 AA; 10032 MW; C4B8AD69078B55FA CRC64;

Query Match 70.1%; Score 118.5; DB 2; Length 89;
Best Local Similarity 40.3%; Pred. No. 1.3e-09;
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSTRCPGCRFFG-----GLKRIQ 23
    |||||
DB 22 KPVSLSTRCPGFESHIRANVXHLKINTPNCALQIVARLKNRNQVCIDPKLXWIOE 81
    |||||
QY 24 YLEKALN 30
    |||||
DB 82 YLEKALN 88

RESULT 7
CAG29279 PRELIMINARY; PRT; 89 AA.
AC CAG29279;
DT 20-MAY-2004 (TrEMBLrel. 27, Created)
DT 20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT 20-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE CXCL12 protein (Fragment).
DE CXCL12
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ebert L., Schick W., Neubert P., Schatten R., Henze S., Korn B.;
RT "Cloning of human full open reading frames in Gateway(TM) system entry
RT vector (pDONR201).";
RL Submitted (MAY-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL: CR450283; CAG29279.1; -.
FT NON_TER
FT 89
SQ SEQUENCE 89 AA; 10103 MW; 62B44EBD209C3A14 CRC64;
Query Match 70.1%; Score 118.5; DB 2; Length 89;

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Best Local Similarity 40.3%; Pred. No. 1.3e-09;  
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GLKWIQ 23  
DB 22 KPVSLSYRCPCRFESHVAVANVHKLINTPNCALQIVARLKNRRQVCIDPRLKWIQ 81

QY 24 YLEKALN 30  
DB 82 YLEKALN 88

## RESULT 8

ID SDPI PRELIMINARY; PRT; 92 AA.

Q9H554  
AC Q9H554; PRELIMINARY;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE BA2015.1.2 (Stromal cell-derived factor 1, isoform beta)  
DE (Fragment).  
GN Name=SDPI;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_Taxid=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA Bird C.;  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL137026; CAC10202.1; -.  
DR HSSP; P48061; ISDF.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0008009; P:chemokine activity; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR002473; C-X-C/Interlkn\_8.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR PRINTS; PR00436; INTERLEUKIN8.  
DR SMART; SM00199; SCY; 1.  
FT NON TER 1  
SQ SEQUENCE 92 AA; 10510 MW; AEF0C402B48B20 CRC64;

Query Match 70.1%; Score 118.5; DB 2; Length 92;  
Best Local Similarity 40.3%; Pred. No. 1.4e-09;  
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GLKWIQ 23  
DB 22 KPVSLSYRCPCRFESHVAVANVHKLINTPNCALQIVARLKNRRQVCIDPRLKWIQ 81

QY 24 YLEKALN 30  
DB 82 YLEKALN 88

## RESULT 9

ID SDPI FELCA STANDARD; PRT; 93 AA.

AC 062657;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).  
GN Name=CXCL12; Synonyms=SDPI;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OC NCBI\_Taxid=9685;  
RN (1)  
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
RC TISSUE=Thymus;  
RX MEDLINE=98450506; PubMed=9777331;

RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K.,  
RA Cai J.S., Sato E., Kohmoto M., Mikami T.;  
RT "Molecular cloning and sequencing of feline stromal cell-derived  
RT factor-1 alpha and beta."  
RL Eur. J. Immunogenet. 25:303-305(1998).  
CC -1- FUNCTION: Chemottractant active on T-lymphocytes, monocytes, but  
CC not neutrophils.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Beta;  
CC IsoId=O62657-1; Sequence=Displayed;  
CC Name=Alpha;  
CC IsoId=O62657-2; Sequence=VSP\_001055;  
CC -1- SIMILARITY: Belongs to the Interleukin alpha (chemokine CXC)  
CC family.

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DR EMBL; AB011966; BA28602.1; -.  
DR HSSP; P48061; ISDF.  
DR InterPro; IPR002473; C-X-C/Interlkn\_8.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR InterPro; IPR001089; CXC\_chemokine\_small.  
DR Pfam; PF00048; IL8; 1.  
DR PRINTS; PR00436; INTERLEUKIN8.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00471; SMALL\_CYTOKINES\_CXC; FALSE NEG.  
KW Alternative splicing; Chemotaxis; Cytokine; Growth factor; Signal.  
FT SIGNAL 1  
FT CHAIN 22  
FT DISULFID 30  
FT DISULFID 32  
FT VARSPIC 90  
FT FTID=VSP\_001055.  
SQ SEQUENCE 93 AA; 10581 MW; 44FC763711E9BE37 CRC64;

Query Match 70.1%; Score 118.5; DB 1; Length 93;  
Best Local Similarity 40.3%; Pred. No. 1.4e-09;  
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GLKWIQ 23  
DB 22 KPVSLSYRCPCRFESHVAVANVHKLINTPNCALQIVARLKNRRQVCIDPRLKWIQ 81

QY 24 YLEKALN 30  
DB 82 YLEKALN 88

## RESULT 10

ID SDPI HUMAN STANDARD; PRT; 93 AA.

AC P48061;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (pre-B cell  
DE growth stimulating factor) (PBSF) (HIRH) [Contains: SDF-1-beta(3-72)];  
GN Name=CXCL12; Synonyms=SDPI;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_Taxid=9606;  
RN (1)  
RP SEQUENCE FROM N.A.

RA Spotila L.D.;  
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96039262; PubMed=7490086;  
 RA Shitizu M., Nakano T., Inazawa J., Tashiro K., Tada H., Shinohara T.,  
 Honjo T.;  
 RT "Structure and chromosomal localization of the human stromal cell-  
 RT derived factor 1 (SDF1) gene."  
 RL Genomics 28:495-500(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
 RC TISSUE=Liver;  
 RA Begum N.A., Barnard G.F.;  
 RT "Nucleotide sequence of hRHR, human intercrine reduced in hepatomas."  
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15164054; DOI=10.1038/nature02462;  
 RA Deloukas P., Barthrowl M.E., Graham D.V., Rubenfeld M., French L.,  
 Steward C.A., Sims S.K., Jones M.C., Searle S., Scott C., Howe K.,  
 Hunt S.B., Andrews T.D., Gilbert J.G.R., Swarbreck D., Ashurst J.L.,  
 Taylor A., Batties J., Bird C.P., Alencough R., Almeida J.P.,  
 Banerjee R., Bates K., Beasley H., Bray-Allen S., Brown A.J.,  
 Brown J.Y., Burford D.C., Burrill W., Burton J., Cahill P., Camire D.,  
 Carter N.P., Chapman J.C., Clark S.Y., Clarke G., Clee C.M., Clegg S.,  
 Corby N., Coulson A., Dhali P., Dutta I., Dunn M., Faulkner L.,  
 Franchet A., Frankland J.A., Garner P., Garnett J., Grable S.,  
 Griffiths C., Grocock R., Gustatson E., Hammond S., Harley J.L.,  
 Hart B., Heath P.D., Ho T.P., Hopkins B., Horne J., Howden P.J.,  
 Huckle E., Hynds C., Johnson C., Johnson D., Kana A., Kay M.,  
 Kimberley A.M., Kershaw J.K., Kokkinaki M., Laird G.K., Lawlor S.,  
 Lee H.M., Leongamornlert D.A., Laird G., Lloyd C., Lloyd D.M.,  
 Loveland J., Lovell J., McLaren S., McLay K.E., McMurray A.,  
 Mashghi-Mohammadi M., Matthews L., Milne S., Nickerson T.,  
 Nguyen M., Overton-Latty E., Palmer S.A., Pearce A.V., Beck A.I.,  
 Pellan S., Phillimore B., Porter K., Rice C.M., Rogosin A., Rose M.T.,  
 Sarafidou T., Shira H.K., Showkhen R., Skuce C.D., Smith M.,  
 Strachan L., Sycamore N., Teater J., Thorpe A., Torcaso W.,  
 Tracey A., Tromans A., Tselas J., Wall M., Walsh J., Wang H.,  
 Weinrock K., West A.P., Willey D.L., Whitehead S.L., Wilming L.,  
 Wray P.W., Young L., Chen Y., Lovering R.C., Moschonas N.K.,  
 Stebert R., Fechtel K., Bentley D., Durbin R., Hubbard T.,  
 Doucette-Stamm L., Beck S., Smith D.R., Rogers J.;  
 RL "The DNA sequence and comparative analysis of human chromosome 10."  
 RL Nature 429:375-381(2004).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Bluetow K.H., Scheet C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Pierce T.E.,  
 Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Scheer T.E.,  
 Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 Hosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.R.,  
 Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butlerfield Y.S.N., Krzywinski M.I., Skalek U., Smalins D.E.,  
 Schnerich A., Schein J.E., Jones S.J.M., Matra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RP IDENTIFICATION OF SDF-1ALPHA(3-67) AND SDF-1BETA(3-72) BY MASS

RP SPECTROMETRY, AND N-TERMINAL AND C-TERMINAL PROCESSING.  
 RX PubMed=14525775; DOI=10.1182/blood-2003-08-2857;  
 RA De la Luz Sierra M., Yang F., Narazaki M., Salvucci O., Davis D.,  
 Yarchan R., Zhang H.H., Fales H., Toato G.;  
 RT "Differential processing of stromal-derived factor-1alpha and beta  
 RT explains functional diversity."  
 RL Blood 103:2452-2459(2004).  
 RN [7]  
 RP STRUCTURE BY NMR OF 22-88.  
 RX MEDLINE=98046030; PubMed=9384579;  
 RA Crump M.P., Gong U.H., Loetscher P., Rajaratnam K., Amara A.,  
 Arenzana-Seisdedos F., Vitellizier J.L., Baggiolini M., Sykes B.D.,  
 Clark-Lewis I.;  
 RT "Solution structure and basis for functional activity of stromal cell-  
 RT derived factor-1; dissociation of CXCR4 activation from binding and  
 RT inhibition of HIV-1."  
 RL EMBO J. 16:6996-7007(1997).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.  
 RX MEDLINE=98284037; PubMed=9618518;  
 RA Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Stani M.A.,  
 Lolite E.;  
 RT "Crystal structure of chemically synthesized [N3A] stromal cell-  
 RT derived factor 1alpha, a potent ligand for the HIV-1 'fusin'  
 RT coreceptor."  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).  
 CC -1- FUNCTION: Chemotactant active on T-lymphocytes, monocytes, but  
 CC not neurophilic. SDF-1-beta(3-72) and SDF-1-alpha(3-67) show a  
 CC reduced chemotactic activity. Binding to cell surface  
 CC proteoglycans seems to inhibit formation of SDF-1-alpha(3-67) and  
 CC thus to preserve activity on local sites.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Beta; Synonyms=SDF-1-beta(1-72);  
 CC IsoId=P48061-1; Sequence=Displayed;  
 CC Name=Alpha; Synonyms=SDF-1-alpha(1-68);  
 CC IsoId=P48061-2; Sequence=VSP\_001056;  
 CC -1- PTM: Processed forms SDF-1beta(3-72) and SDF-1alpha(3-67) are  
 CC produced after secretion by proteolytic cleavage of isoforms Beta  
 CC and Alpha, respectively. The N-terminal processing is probably  
 CC achieved by DPP4. Isoform Alpha is first cleaved at the C-terminus  
 CC to yield a SDF-1-alpha(1-67) intermediate before being processed  
 CC at the N-terminus. The C-terminal processing of isoform Alpha is  
 CC reduced by binding to heparin and, probably, cell surface  
 CC proteoglycans.  
 CC -1- SIMILARITY: Belongs to the intercrine alpha (chemokine Cxk)  
 CC family.  
 CC -----  
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC -----  
 CC EMBL: U16753; AAA97434.1; -;  
 CC EMBL: L36033; AAB39332.1; -;  
 CC EMBL: L36034; AAB39333.1; -;  
 CC EMBL: U19495; AAB40516.1; -;  
 CC EMBL: AL137026; CAC10203.1; -;  
 CC EMBL: BC039893; AAH39893.1; -;  
 CC PIR: G01540; G01540.  
 CC PDB: 1A15; X-ray; A/B=22-88.  
 CC PDB: 1OG7; X-ray; A/B=22-88.  
 CC PDB: 1SDP; NMR; @=22-88.  
 CC PDB: 2SDP; NMR; @=22-88.  
 CC Genew; HGNC:10672; CXCL12.  
 CC MIM: 600835; -;  
 CC GO: GO:0008009; F:chemokine activity; TAS.  
 CC GO: GO:0005102; F:receptor binding; TAS.  
 CC GO: GO:0006874; P:calcium ion homeostasis; TAS.

DR	GO:0007155	P:cell adhesion;TAS.
DR	GO:0006935	P:chemotaxis;TAS.
DR	GO:0008015	P:circulation;TAS.
DR	GO:0007186	P:g-protein coupled receptor protein signalin. . .;TAS.
DR	GO:0006955	P:immune response;TAS.
DR	GO:0008054	P:regulation of actin polymerization and/or d. . .;TAS.
DR	GO:0009615	P:response to virus;TAS.
DR	GO:0007165	P:signal transduction;TAS.
DR	InterPro: IPR002473	C-X-C/Interlkn_8.
DR	InterPro: IPR01811	Chemokine_118.
DR	InterPro: IPR01089	CXC_chemkine_sm11.
DR	Pfam: PF00048	IL8; 1.
DR	PRINTS: PR00436	INTERLEUKIN8.
DR	PROSITE: PS00471	SMALL CYTOKINES CXC; FALSE NEG.
KM	3D-structure; Alternative splicing; Chemotaxis; Cytokine;	
KM	Growth factor; Signal.	
FT	SIGNAL	1
FT	CHAIN	22
FT	CHAIN	24
FT	CHAIN	24
FT	DISULFID	30
FT	DISULFID	32
FT	VARSPLIC	90
FT	STRAND	36
FT	HELIX	41
FT	STRAND	44
FT	TURN	53
FT	STRAND	59
FT	TURN	64
FT	STRAND	69
FT	TURN	74
FT	HELIX	77
FT	TURN	83
FT	HELIX	84
SO	SEQUENCE	93 AA; 10666 MW; 505B5A29C2B44EBD CRC64;
Query Match		
Best Local Similarity		
Matches		
27; Conservative		
70.1%; Score 118.5; DB 1; Length 93;		
40.3%; Pred. No. 1.4e-09;		
0; Mismatches		
3; Indels		
37; Gaps		
QY	1 KPVSLSYRCPGPRFGG-----GLKWIQ	23
DB	22 KPVSLSYRCPGFRESHVAVRANVGLKLINTPNCALQIVARLKNRRVQCIDPKLKWIOE	81
QY	24 YLEKALN 30	
DB	82 YLEKALN 88	
RESULT 11		
ID	Q6EKW4	PRELIMINARY; PRT; 116 AA.
AC	Q6EKW4;	
DT	01-OCT-2004 (TREMBLrel. 28; Created)	
DT	01-OCT-2004 (TREMBLrel. 28; Last sequence update)	
DT	01-OCT-2004 (TREMBLrel. 28; Last annotation update)	
DE	CXCL12 chemokine.	
GN	Name=CXCL12;	
OS	Sus scrofa (Pig).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
OX	NCBI_TaxId=9823;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	Pubmed=15242943;	
RA	Leader T.N., Pinton P., Bourges D., Roumi P., Salmon H., Oswald I.P.;	
RT	"Development of a macroarray to specifically analyze immunological	
RT	gene expression in swine."	
RL	Clin. Diagn. Lab. Immunol. 11:691-698 (2004).	
EMBL	AY312066; AA084094.1.-.	
SEQ	SEQUENCE 116 AA; 12622 MW; 2A1BC0551C2BBAB CRC64;	

Query Match	70.1%	Score 118.5	DB 2	Length 116
Best Local Similarity	40.3%	Pred. No. 1.7e-09		
Matches 27	Conservative 0	Mismatches 3	Indels 37	Gaps

  

Qy	1	KPVSLSYRCPCRFEGG-----	GIKWTIOE 23
Db	22	KPVSLSYRCPCRFEGSHVARANIKHLINTPCALQIVARLKSNNRQCIDPKLKWIOE 81	
Oy	24	YLERKALN 30	
Db	82	YLERKALN 88	

  

RESULT 12	Q80ZM4	PRELIMINARY;	PRT;	137 AA.
ID	Q80ZM4			
AC	Q80ZM4			
DT	01-JUN-2003 (TrEMBLrel. 24, Created)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DS	Cxcl12 protein.			
DN	Cxcl12			
OS	Mouse			
OC	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
CK	NCBI_TaxID=10090;			
[1]	SEQUENCE FROM N.A.			
RP	STRAIN=C57BL/6; TISSUE=Brain;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schlier G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Dicciencio L., Marinska K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stadlton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Rana S.S., Loguellano N.A., Peters G.U., Abramson R.D., Mallaby S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield J.E.,			
RA	Kryzhanovskii M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6; TISSUE=Brain;			
RA	Strausberg R.,			
RL	Submitted (Feb-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC046827; AA046827.1; -.			
DR	HSSP; P48061, 1SDP.			
DR	MGI; MGI:103556; Cxcl12.			
DR	GO; GO:0008009; F:chemokine activity; IDA.			
DR	GO; GO:0007420; P:brain development; IDA.			
DR	GO; GO:0007281; P:germ cell development; IDA.			
DR	GO; GO:0008354; P:germ cell migration; IDA.			
DR	GO; GO:0005030; P:induction of positive chemotaxis; IDA.			
DR	GO; GO:0030335; P:positive regulation of cell migration; IDA.			
DR	GO; GO:0042098; P:T-cell proliferation; IMP.			
DR	InterPro; IPR002473; C-X-C/Interln_8.			
DR	InterPro; IPR01811; Chemokine_IL8.			
DR	Pfam; PF00048; IL8; 1.			
DR	PRINTS; PR00436; INTERLEUKIN8.			
DR	SMART; SMO0199; SCY, 1.			
SD	SEQUENCE 137 AA; 15529 MW; 04B47DAB6904DF77 CRC64;			

  

Query Match	70.1%	Score 118.5	DB 2	Length 137
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Best Local Similarity 40.3%; Pred. No. 2e-09;  
Matches 27; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----LKWIOE 23  
|||||  
DB 22 KPVSLTYRCPCRFESNVARANIKILSTPNCSLQIVARLKSNSKQVCIDPKLKWIOE 81  
|||||

QY 24 YLEKALN 30  
|||||  
DB 82 YLEKALN 88

## RESULT 13

Q6T7C0 PRELIMINARY; PRT; 89 AA.

AC Q6T7C0;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DE Stromal cell-derived factor-1 alpha.  
GN Name=SDP1;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Raz B., Stebler J.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TTSUE=SpLeen;  
RA Read L.R., Cumberbatch J., Sharif S.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY429472; AAR91695.1; -;  
DR EMBL; AY451855; AAR8102.1; -;  
DR InterPro; IPR002473; C-X-C/Interlkn\_8.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR PRINTS; PR00436; INTERLEUKIN8.  
DR SMART; SM00199; SCY; 1.  
SQ SEQUENCE 89 AA; 10104 MW; 21E53D121A557965 CRC64;

Query Match 69.5%; Score 117.5; DB 2; Length 89;  
Best Local Similarity 38.8%; Pred. No. 1.8e-09;  
Matches 26; Conservative 1; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----LKWIOE 23  
|||||  
DB 22 KPVSLTYRCPCRFESNVARANIKILSTPNCSLQIVARLKSNSKQVCIDPKLKWIOE 81  
|||||

QY 24 YLEKALN 30  
|||||  
DB 82 YLEKALN 88

## RESULT 14

AAR8102 PRELIMINARY; PRT; 89 AA.

AC AAR8102;  
DT 02-MAR-2004 (TReMBLrel. 27, Created)  
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)  
DE Stromal cell derived factor 1.  
GN SDF1.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.

RC TTSUE=SpLeen;  
RA Read L.R., Cumberbatch J., Sharif S.;  
RL "Characterization of Chicken SDF-1";  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY451855; AAR8102.1; -;  
SQ SEQUENCE 89 AA; 10104 MW; 21E53D121A557965 CRC64;

QY 1 KPVSLSYRCPCRFEGG-----LKWIOE 23  
|||||  
DB 22 KPVSLTYRCPCRFESNVARANIKILSTPNCSLQIVARLKSNSKQVCIDPKLKWIOE 81  
|||||

QY 24 YLEKALN 30  
|||||  
DB 82 YLEKALN 88

## RESULT 15

AAR91695 PRELIMINARY; PRT; 89 AA.

AC AAR91695;  
DT 14-APR-2004 (TReMBLrel. 27, Created)  
DT 14-APR-2004 (TReMBLrel. 27, Last sequence update)  
DT 14-APR-2004 (TReMBLrel. 27, Last annotation update)  
DE Stromal cell-derived factor-1 alpha.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Raz B., Stebler J.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY429472; AAR91695.1; -;  
SQ SEQUENCE 89 AA; 10104 MW; 21E53D121A557965 CRC64;

Query Match 69.5%; Score 117.5; DB 2; Length 89;  
Best Local Similarity 38.8%; Pred. No. 1.8e-09;  
Matches 26; Conservative 1; Mismatches 3; Indels 37; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----LKWIOE 23  
|||||  
DB 22 KPVSLTYRCPCRFESNVARANIKILSTPNCSLQIVARLKSNSKQVCIDPKLKWIOE 81  
|||||

QY 24 YLEKALN 30  
|||||  
DB 82 YLEKALN 88

Search completed: January 4, 2005, 15:49:53  
Job time : 61.541 secs